

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 10, 2003, 08:10:41, Search time 5750 Seconds

3671.194 Million cell updates/sec

Title: US-09-820-790b-2

Perfect score: 2715
Sequences: 1 MATVCTCFRPFQVHDI.....DEFWNWFCSAFVAF516

Scoring table: BLOSUM62
Xgapop 10.0 Xgapext 0.5
Ygapop 10.0 Ygapext 0.5
Fgapop 6.0 Fgapext 7.0
Delop 6.0 Delext 7.0

Searched: 2888711 seqs, 204461386 residues

Total number of hits satisfying chosen parameters: 577722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-USPOP=pool/US88830/rnaus_081003_17018.1176/-pp-gnssr.fasta.1.711
-UNITES-bits -FARG-1 -REQ-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-SOCIALIGN=200 -THR_SCORE=pet -THR_MAX=100 -THR_MIN=0 -ACTION=15 -MODE=LOCAL
-USPR=US88820790.EGNA.1.3635.rnaus_0910203.17018.11763 -NCPOP=6 -ICPU=3
-NO_MAP -LARGQUERY -NEI_SCORES=0 -WAT -DISPLOCK=100 -LONGLOC
-DEV=USPOP=pool/US88830/rnaus_081003_17018.1176/-pp-gnssr.fasta.1.711
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-MARGEN-7

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3: gb-la.*

4: gb-cc.*

5: gb-om.*

6: gb-jst.*

7: gb-ph.*

8: gb-ec.*

9: gb-er.*

10: gb-ro.*

11: gb-at.*

12: gb-gt.*

13: gb-un.*

14: gb-vi.*

15: gb-ye.*

16: sm-fun.*

17: sm-hum.*

18: sm-lin.*

19: sm-mus.*

20: sm-om.*

21: sm-ov.*

22: sm-ort.*

23: sm-pl.*

24: sm-ph.*

25: sm-pl.*

26: sm-ye.*

27: sm-ye.*

28: sm-un.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2692	99.2	127	9 AF078803	X078803 Homo sapi
3	2672	98.4	3630	10 MCMAMK2	X63615 Mus muscu
4	2669	98.3	1840	10 RARFCA	M6112 Rat brain t
5	2669	98.3	1840	10 RARFCA	M6112 Rat brain t
6	2571	94.7	2270	9 AF081520	AF081520 Homo sap
7	2571	94.7	1703	5 AF085249	AF085249 Gallus ga
8	25249	93.9	1257	9 HS252238	A252238 Homo sapi
9	25249	93.9	1257	9 HS252238	A252238 Homo sapi
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29	2235	82.0	2384	5 AF233633	A233633 Xenopus l
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31	22223	81.9	1829	4 D1495	D14955 Cryptalaus
32	2216	81.6	1764	10 S71570	S71570 Oryz-palmod
33	2215	81.2	1823	10 AF358864	AF358864 Mus muscu
34	2215	81.2	1823	10 AF358864	AF358864 Mus muscu
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44	2077	76.5	1705	9 BC032784	BC032784 Homo sapi
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ALIGNMENTS

RESULT 1

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[illegible]

[illegible]

[illegible]

[illegible]

HPA (HTMA-) HTMAN GENOME SCT INC.

XX
OUT TO BROWNS STREET (BROW)

PI Rosen CA, Barash

XX

WPI: 2001-581633/65.
P-PSDB: AAU87358.

XX

Claim 1: SEQ ID NO 278; 837pp: English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein, (3) and polypeptides (III) encoded by (I), are used to treat a medical condition and in diagnosis of autoimmune diseases e.g. Rheumatoid arthritis, hypersplenofoliarative include disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, myelographic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastroenteritis and disorders e.g. typhus, and disorders e.g. testicular feminization, endocrine disorders e.g. diabetes and pituitary tumours, cancers and disorders at the cellular level e.g. cancer, and disorders e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotherapy. The polypeptides can decrease foreign antibody binding to surface ligands, e.g. receptors.

Search completed: October 10, 2003, 04:14:28
Job time : 645 secs

[illegible]

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RESULT 4

Sequence 14, Application US/9272796

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Giesler, Karl G.
 APPLICANT: Lutz, Preseli
 APPLICANT: Lutz, Preseli K.
 APPLICANT: Shah, Parvati
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 TITLE OF INVENTION: KINASES
 ADDRESS: 110101
 CORRESPONDENCE ADDRESS:
 ADDRESS: 110101
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTED For Windows Version 2.0
 CURRENT APPLICATION DATA: US/9272796
 FILING DATE: 05/09/2003
 CLASSIFICATION:
 PREVIOUS APPLICATION DATA:
 FILING DATE: 06/07/99
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J J
 REGISTRATION NUMBER: 36,749
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 12:
 SOURCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDNESS: single
 IMMEDIATE SOURCE:
 CLONE: 827431

Query Match

Best Local Similarity 52.8%; Pred. No. 4.4e-37;
 Matches 475; Conservative 415; Idicals 122; Gaps 3;
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 DB 1061 TGGGAGAGCTGACGGGAGAGCTTACCGGAGAGACTGCTTCGGGAGAGTGA 1117


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1  NUMBER OF SEQUENCES: 94
2  CORRESPONDENCE ADDRESS:
3  INVENTOR: Ciba-Geigy Corporation
4  STREET: 7 Sylvline Drive
5  CITY: Hawthorne
6  STATE: New York
7  ZIP: 10532
8
9  COMPUTER READABLE FORM:
10  FILE NAME: 09-820-790b-1.ln1
11  COMMENTS: IBM PC compatible
12  OPERATING SYSTEM: PC-DOS/MS-DOS
13  SOFTWARE: Patent Release #1.0, Version #1.30B
14  APPLICATION NUMBER: US/07/951,715A
15  FILING DATE: 25-SEP-1992
16  PRIORITY DATE: 25-SEP-1992
17  PRIORITY NUMBER: US 07/951,715
18  PRIORITY DATE: 25-SEP-1992
19  PRIORITY NUMBER: US 07/772,027
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21  PREVIOUS APPLICATION DATA:
22  APPLICATION NUMBER: US 07/772,027
23  FILING DATE: 04-OCT-1991
24  PRIORITY DATE: 04-OCT-1991
25  PRIORITY NUMBER: US 07/772,027
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27  NAME: Spruill, W. Murray
28  REGISTRATION NUMBER: 32,943
29  TELEPHONE: (919)541-8615
30  TELECOMMUNICATION INFORMATION:
31  TELEFAX: (919)541-8689
32  LENGTH: 1349 base pairs
33  SEQUENCE CHARACTERISTICS: 20:
34  STRANDEDNESS: single
35  TOPOLOGY: linear
36  MOLECULE TYPE: cDNA
37  ORGANISM: Homo sapiens
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39  NAME/KEY: CDS
40  LOCATION: 1..1349
41  OTHER INFORMATION:
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44  OTHER INFORMATION: disclosed in Figure 30."
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46  US-07-951-715A-20
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48  Query Match
49  Best Local Similarity 55.24; Pred. No. 6,6e-32;
50  Matches 459; Conservative 0; Mismatches 933; Indels 6; Gaps 2;
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[illegible]

Search completed: October 10, 2003, 07:50:51
Job time : 155 secs

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RESULT 8
 US-09-925-299-210 Application US/09925299
 Sequence 210, Application US/09925299
 Patent No. US6020055E27A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: P102
 CURRENT APPLICATION NUMBER: US/09/925,299
 PRIORITY DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: US/08/05883
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 NUMBER OF SEQ ID NOS: 1556
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1551
 LENGTH: 1551
 TYPE: DNA
 ORGANISM: Homo sapiens
 NAME/FEATURE
 LOCATION: (760)
 NAME/FEATURE: n equals a.t.g. or c
 LOCATION: (1543)
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 LOCATION: (1544)
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 LOCATION: (1551)

Query Match. 27.5%; Score 610.2; DB 9; Length 1551;
 Best Local Similarity 78.0%; Fred. No. 5.2e-151;
 Matches 744; Conservative 2; Mismatches 206; Indels 2; Gaps 1;
 QY 262 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 321
 DB 489 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 548
 QY 322 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 381
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DB 729 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 788
 QY 560 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 619
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 DB 1389 ATCAAGAGCTGATGAGCTGAGAGACACCGGCGTCTGCGACAGCTCCAGTAC 1442

RESULT 9
 US-09-925-299-210
 Sequence 210, Application US/09925299
 Patent No. US6020055E27A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: P102
 CURRENT APPLICATION NUMBER: US/09/925,299
 PRIORITY DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: US/08/05883
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 NUMBER OF SEQ ID NOS: 1556
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 210
 LENGTH: 1551
 TYPE: DNA
 ORGANISM: Homo sapiens
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 LOCATION: (1543)
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 NAME/FEATURE: n equals a.t.g. or c
 LOCATION: (1547)
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 LOCATION: (1548)
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 LOCATION: (1549)
 NAME/FEATURE: n equals a.t.g. or c
 LOCATION: (1550)
 NAME/FEATURE: n equals a.t.g. or c
 LOCATION: (1551)

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Db	1374	AGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	160	Db	224	TACATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	165
Qy	1304	AGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	1245	Qy	495	ATTTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	514
Db	1361	ATATTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	180	Db	164	CGTGGAGCGCTCTTCATCTTCCACCAATGCGGGCTCTCCACAGAGGAGGACCGGAG	105
Qy	1244	CGTGGAGCGCTCTTCATCTTCCACCAATGCGGGCTCTCCACAGAGGAGGACCGGAG	1185	Qy	515	TTTTTT	515
Db	1381	AGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG	200	Db	104	CTGCGAG	99
Qy	1184	CGTGGAGCGCTCTTCATCTTCCACCAATGCGGGCTCTCCACAGAGGAGGACCGGAG	1125	Db	104	CTGCGAG	99
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RESULT 4

AAZ45160 standard; cDNA: 2110 bp.

AAZ45160:

AC AAZ45160:

AC AAZ45160:

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[illegible][illegible]

[illegible]

PT Combination for diagnosing, staging, treating, or monitoring the
PT progression of treatment of a vascular disease, e.g. atherosclerosis,
PT comprises several CNAs that are differentially expressed in activated
PT vascular tissue.-

DS
XX
Claim 1: Page - : 1800: English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have any of the following functions: (i) they may be used as diagnostic, prognostic, epidemiological, virologic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high throughput method for detecting differential expression of one or more genes. The cDNAs of the invention may be used to specifically identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compound to identify a ligand that specifically binds to a cDNA of the invention. The cDNA of the invention may be used that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of coronary artery disease, hypertension, diabetes, pre-eclampsia, tachycardia, reperfusion injury, stenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new genes. The cDNAs of the invention may be used to identify new cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence of the cDNA of the invention that is differentially expressed in activated vascular tissue.

CC activated vascular tissue.
CC Note: The sequence data for this patent did not form part of the
CC specification, but was obtained in electronic format directly from USPTO
CC at <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>.

Sequence 3705 BP; 901 A; 961 C; 970 G; 873 T; 0 other;

Alignment Scores:

Pred. No.:	9.5e-193	Length:	3705
Score:	2186.50	Matches:	421
Percent Similarity:	81.18%	Conservative:	19
Best Local Similarity:	77.68%	Mismatches:	29
Query Match:	80.53%	Indels:	73
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US-09-820-790B-2 (1-516) X ABX63227 (1-3705)

[illegible][illegible]

TITLE	JOURNAL	COMMENT
1781	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Full-length cDNA libraries and normalization
1782	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Unpublished
1783	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Contact: Genoscope
1784	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Genoscope, National de Sequences
1785	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	BP 191 91005 RPRY cadex France
1786	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1787	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Library was constructed by life technologies, a division of
1788	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	Genoscope, no sequence cluster 3877.r for
1789	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	more information about this cluster, see
1790	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	http://www.genoscope.cns.fr/
1791	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	seqref@genoscope.cns.fr
1792	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	seqref@genoscope.cns.fr
1793	AAAGCTGTGACATCAACCTTCCACAGCTATCAACAGCTCTGAGCGCTTGAACACCA	http://fuller.hi.invitrogen.com/invitrogen Corporation 1600
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QY      114  SerGlnIyGlnIleGlnIleuAlaIyGslYgAlaIrgGlyGlnValIys 133
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Db      666  CAGCGAGGAGCTACCGCGAGAGATCTTATCTACGTACGACAGAGAGAGGTCGAAATA 725
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RSLMT 3

US-09-620-3120-526

; Sequences 526; Application US/09620312D

; Sequences 526; Application

; GENERAL INFORMATION:

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; APPLICANT: Tang, Y. Tom
; APPLICANT: Lito, Chinghua
; APPLICANT: Sheng, Jie
; APPLICANT: Sheng, Jie
; APPLICANT: Ren, Feiyao
; APPLICANT: Chen, Rui-hong
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aigong J.
; APPLICANT: Xue, Aigong J.
; APPLICANT: Wang, Jia-Bin
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuchang
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillophast
; APPLICANT: John Tillophast
; TITLE OF INVENTION: Polypeptides
; FILE OF INVENTION: No. 0666261 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09-620-312D
; PRIOR FILING DATE: 2000-07-19
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; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 1105
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; FEATURE:
; NAME/KEY: CDS
; ORIGIN: 1 (1372)
US-09-620-3120-526

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Alignment Scores: 2,366-57
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Percent Similarity: 54.13%
Best Local Similarity: 25.73%
Conservative: 69
Mismatch: 125
Gaps: 6

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QY      114  SerGlnIyGlnIleGlnIleuAlaIyGslYgAlaIrgGlyGlnValIys 133
Db      578  AGACCTCTATCGCGAGGCTCGGAGGCGCTACTACTCTACAGAGATGGCATGTC 637
QY      134  HisArgGlnIyPheProGlnuIleuIeuIalSerIleuIalSerIyGlnIyAlaVal 153
Db      637  CAGCGAGGAGCTACCGCGAGAGATCTTATCTACGTACGACAGAGAGAGGTCGAAATA 696

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Db 638 CAGAGAGCTGACGACCGGAAATCTTCTACTACGATGAGAGGAGGATCGAATA 597
Qy 154 jylwlelaphedlphedlphedlphedlphedlphedlphedlphedlphedl 173
Db 698 ATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754
Qy 174 Phalaphedlphedlphedlphedlphedlphedlphedlphedlphedl 193
Db 795 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
Qy 194 Frowalaphedlphedlphedlphedlphedlphedlphedlphedlphedl 213
Db 815 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
Qy 214 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 233
Db 875 TTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 734
Qy 234 Frowalaphedlphedlphedlphedlphedlphedlphedlphedlphedl 253
Db 935 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 794
Qy 254 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 273
Db 995 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854
Qy 274 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 293
Db 1095 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1114
Qy 294 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 311
Db 1175 TTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
Qy 312 Frowalaphedlphedlphedlphedlphedlphedlphedlphedlphedl 331
Db 1172 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1231
Qy 332 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 351
Db 1220 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
Qy 352 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 371
Db 1280 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1339
Qy 372 Phedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 386
Db 1340 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360

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RESULT 4: 226-3

Sequence 3, Application US/09/57326

Patent No. 647210

ORIGINATOR INFORMATION: C. Alexander Jr.

APPLICANT: Nathan, Brian

TITLE OF INVENTION: No. 647210 Human Kinases and Polynucleotides Encoding the Same

CURRENT FILING DATE: 2001-10-11

CURRENT FILING DATE: 2001-10-11

NUMBER OF SEQ. ID NOS.: 10-12

SOFTWARE: FASTSEQ for Windows version 4.0

SEQ ID NO. 3

TYPE: DNA

ORIGINATOR: homo sapiens

US-09-573-326-3

Alignment Scores:

Pred. No.: 2298

Score: 586.50 Matches: 139
Percent Similarity: 53.47% Conservation: 69
Query Match: 21.60% Gaps: 2
Gaps: 4

US-09-820-790b-2 (1-516) x US-09-973-326-3 (1-2298)

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Qy 12 Aspetyrthylphedlphedlphedlphedlphedlphedlphedlphedlphedl 139
Db 1171 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1230
Qy 32 Valysylphedlphedlphedlphedlphedlphedlphedlphedlphedl 51
Db 1231 ATGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1290
Qy 52 Alaphedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 71
Db 1232 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1347
Qy 72 Asilphedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 91
Db 1233 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
Qy 92 Levalthylphedlphedlphedlphedlphedlphedlphedlphedlphedl 111
Db 1408 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
Qy 112 Asilphedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 131
Db 1468 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1527
Qy 132 Valysylphedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 151
Db 1528 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
Qy 152 ---Alaphedlphedlphedlphedlphedlphedlphedlphedlphedlphedl 170
Db 1588 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Qy 171 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190
Db 1639 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1968
Qy 191 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 210
Db 1699 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1798
Qy 211 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 228
Db 1799 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1818
Qy 229 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
Db 1819 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1878
Qy 249 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 268
Db 1879 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1938
Qy 269 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 286
Db 1939 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1998
Qy 289 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 308
Db 1999 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2058
Qy 309 Levalthylphedlphedlphedlphedlphedlphedlphedlphedlphedl 326
Db 2059 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2118
Qy 326 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342

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11 ThrAspGlyTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAlaArgAsp 30
 123456789101112131415161718192021222324252627282930
 266 ATrpGluValGluTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 35
 31 GysValAlaGluTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 50
 32 GysValAlaGluTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 65
 326 GCGAGGAGCGAG 70
 371 SerAlaGluAspIleuValPheValAlaPheSerValAlaPheSerValAlaPhe 95
 371 GAG 60
 67 LeuLeuValSerAsnIleuValPheValAlaPheSerValAlaPheSerValAlaPhe 86
 431 AGGAG 40
 87 PheValAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSerValAla 106
 491 TTTACTCTCTGAG 50
 107 ThrTrpGluValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 126
 551 TACTATGAG 60
 127 CysGluGluValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 146
 611 TTTGCTCTCTGAG 60
 147 LysCysValAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSerVal 166
 671 GCGAG 70
 731 GTCATCATGAG 781
 187 ArgIleuValAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSerVal 206
 782 GCGAG 841
 207 LeuValAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSerVal 220
 842 CTTCTCTGAG 901
 221 -----LysLeuValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 921
 901 GATAG 961
 239 AspTrpValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 258
 951 -----LysLeuValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 1021
 952 GATAG 1021
 1022 CCGAG 1075
 279 AlaSerValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 296
 1076 GTCGAG 1132
 297 ArgTrpValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 316
 1133 AGGAG 1192
 317 GlyArgGlnTrpAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSer 1258
 1193 GAG 1288
 339 AlaAlaSerValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 366
 1253 GTCGAG 1312

347 -----LysValAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSer 359
 1313 GTCGAG 372
 360 LysAlaSerValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 376
 373 AG 432
 377 LysLeuValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAlaPhe 395
 1433 TACTCTCTGAG 471
 396 ArgSerAlaSerValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAla 414
 1472 GAG 531
 415 LysLeuValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAlaPhe 434
 1532 GTCGAG 452
 435 PheTrpValTrpGlnLeuTyrGluAspIleuValPheValAlaPheSerValAlaPhe 452
 1577 GCGAG 466
 453 LeuAlaPheSerValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 472
 1637 GAG 490
 473 ThrGlnTrpLeuValAlaPheSerValAlaPheSerValAlaPheSerValAlaPhe 492
 1673 -----GTCGAG 492
 481 -----ArgValTrpLeuValAlaPheSerValAlaPheSerValAlaPheSerVal 502
 1712 GTCGAG 502
 503 -----GTCGAG 502
 1763 GATAG 522
 514 Pro 314
 1823 CCG 4825
 8509-620-3120-19
 : Sequence 19, Application US/09603120
 : Patent No. 6569602
 : APPLICANT: Yang, Y. Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Ren, Feiyun
 : APPLICANT: Chen, Rui-hong
 : APPLICANT: Xue, Aizong J.
 : APPLICANT: Tang, Tonghong
 : APPLICANT: Zhou, Ping
 : APPLICANT: Ma, Yuning
 : APPLICANT: Wang, Zhong
 : APPLICANT: Jiao, Jiliang
 : APPLICANT: Duan, Rong
 : APPLICANT: Wang, Jie
 : TITLE OF INVENTION: Polyphosphides
 : FILE REFERENCE: 784CIP28
 : CURRENT APPLICATION NUMBER: 09/09/620-3120
 : PRIORITY DATE: 09/09/99
 : PRIOR APPLICATION NUMBER: 09/552-317
 : PRIOR FILING DATE: 2000-04-25


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OY 94 7HNGYGLYGLUEPHGLUASPIEVALAVALAGLNUITYRSECUJALAEAPALA 113
DB 480 AAGCGTGTGGAGCGCTTTACCGCATGACGAGCGAGCGCGCTCTACAGUAGAGATCG 539
OY 114 SEHISGYSIEDGIDILIELEUJALUAEUJISYSEHGLUWGLYVAL 133
DB 540 AGACATCTGGGTCAGGCTCTGGCGCTCTCTACGTCAGCGACGCTGGGATCTG 599
OY 134 HSLAAGAGAGGTCAGGCTCTGGCGCTCTCTACGTCAGCGACGCTGGGATCTG 599
DB 600 CAGCGGAGCGCTCAGCGAGGAGGAGGCTCTCTACGTCAGCGACGCTGGGATCTG 659
OY 154 LYSLEUAAAPHEPGLUEHALLIEUJISYSEHGLUWGLYVAL 173
DB 660 ATGTCCTGCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 710
OY 174 PHALA--GLYTHRPROGLYTYRLEUASERPROGLUWGLYVALAEUJISYGLY 192
DB 711 AACGCTCTGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 770
OY 193 LYSPLAAGLAPLETAPLAEUJISYSEHGLUWGLYVALAEUJISYGLYTYR 212
DB 771 AACGCTCTGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 830
OY 213 PROPHETPASPGLUAGGIDISYSEHGLUWGLYVALAEUJISYGLYTYR 232
DB 831 CGLYTHRPROGLYTYRLEUASERPROGLUWGLYVALAEUJISYGLYTYR 890
OY 233 PHROFROFROFROFROFROFROFROFROFROFROFROFROFROFROFROFRO 950
DB 891 TTTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 950
OY 253 LEUHLIRLEANPROGLYTHRGLYTHRALHSLALAEUJISYSEHGLUWGLYVAL 1010
DB 951 CUSGAGCGAGCTCTCAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1010

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NAME: 15

US-08-464-164-1

Sequence 1, Application US/08464164

Patent No. 5614195

Applicant: Tansley, Fiona M.

Applicant: Dunn, Paul P. J.

Applicant: Vermilion, Arco

Title of Invention: Occidiosis poultry vaccine

Number of Sequences: 10

Address: 1400 Piccard Drive, Suite 206

State: Maryland

Country: U.S.A.

Zip: 20850

Medium Type: floppy disk

Computer: IBM PC compatible

Operating System: PC-DOS/MS-DOS

Current Application Data: Version 41.25

Applicant Application Number: US/08464164

Classification: 1995

Attorney/Agent Information:

Name: Gortley, Mary E.

Address: 1400 Piccard Drive, Suite 206

Telephone: (301) 258-5200

Investigator: 1

Sequence: 1

Length: 1400 base pairs

Type: nucleic acid

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STRANDNESS: double
TOPOLG: linear
HYPOPHOSPHATE: CHA to mNA
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORGANISM: Eimeria maxima
STRAIN: Roughon
COUNTRY: Maryland
LIBRARY: sporozoite cDNA cloned in Lambda ZAPRI
IMMEDIATE SOURCE: sporozoite
CLONE: En70-1
NAME/KEY: CUS
LOCATION: 1..1368
US-08-464-164-1
Alignment Scores:
Pred. No.: 6,11e-48
Length: 1400
Percent Similarity: 47.65%
Conservative: 94
Mismatch: 156
Blast Local Similarity: 28.43%
Blast Match: 19.46%
Blast Gap: 130
US-09-820-790b-2 (4-56) x US-08-464-164-1 (1-1400)
OY 31 CYEVALISYSEUPEHGLYSEHGLUWGLYVALAEUJISYGLYVAL 90
DB 34 TCGAGCGAGCATACAGCGAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTAC 93
OY 51 SEZALAGY---ASPHISGLINYSLEHGLUWGLYVALAEUJISYGLYSEUPEHGLY 69
DB 94 AAGCGAGCGAGCGAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 153
OY 70 HISEASLEUJISYSEHGLUWGLYVALAEUJISYGLYSEUPEHGLYSEUPEHGLY 89
DB 154 CAGTCAAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 213
OY 90 PHASPEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLY 209
DB 214 AAGCGAGTACGAGGAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 373
OY 110 GLYHAPLAEUJISYSEHGLUWGLYVALAEUJISYGLYSEUPEHGLYSEUPEHGLY 129
DB 274 GAGCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 333
OY 130 MACHYVALHAPLAEUJISYSEHGLUWGLYVALAEUJISYGLYSEUPEHGLYSEUPEHGLY 149
DB 334 AATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 393
OY 150 GLYHAPLAEUJISYSEHGLUWGLYVALAEUJISYGLYSEUPEHGLYSEUPEHGLY 169
DB 394 GAGTCAAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 450
OY 170 ALSTPPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLY 189
DB 451 AATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 507
OY 190 ALSTPPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLY 209
DB 508 AATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 567
OY 220 GLYHAPLAEUJISYSEHGLUWGLYVALAEUJISYGLYSEUPEHGLYSEUPEHGLY 259
DB 568 GAGTCAAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 627
OY 230 ALSTPPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLYSEUPEHGLY 249
DB 628 AATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 687
OY 250 AAGCGAGTACGAGGAGGATTCGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 697

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Query Match: 100.00%
DB: 12
Totals: 0
Gaps: 1

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OY 1 MetAlaThrValThrValThyCysThrArgPheThrAspGluValGlyLeuValGlyAspLeu 20
DB 262 ATGCCACACAGAGTGTGTGATGACGCTCCGCTCCGACGAGGATCCATCTGACGAGGAT 321
OY 21 GlyValGlyAlaPheSerValAlaArgCysValGlyValGlyValGlyValGlyValGly 321
DB 322 GCGACGGGGCTTCTCTGTGTGTGCGAGCTGTGTGTGCACTGTGTGTGCACTGTGTGTGCA 381
OY 41 AlaAlaGlyIleThrLeuThrIleValLeuSerAlaArgAspGlnSerValGlyLeuGly 60
DB 392 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
OY 61 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
DB 442 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
OY 81 SerGluGlyIlePheIleThrValPhePheLeuValThrGlyGlyLeuPheLeu 100
DB 502 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
OY 101 AspIleValThrGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyValGly 120
DB 562 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621
OY 121 LeuGluAlaLeuGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 140
DB 622 CTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 681
OY 141 MetGluGluLeuGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 160
DB 682 AACCTGCTCTGGCAGCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 741
OY 161 AlaAlaGlyValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 180
DB 742 GATCATGAGTGTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 801
OY 181 LeuSerProGluValLeuGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 200
DB 802 GTGTCCCTGAGCTGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
OY 201 GlyValIleThrValLeuValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 220
DB 862 GGGGTGATCTGTACATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 921
OY 221 LysAlaGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 240
DB 922 AACCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 981
OY 241 ValThrProGluValLeuValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 260
DB 982 GTGCTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1041
OY 261 ThrAlaAlaGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 280
DB 1042 ATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1101
OY 281 MetMetIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 300
DB 1102 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1161
OY 301 LysGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 320
DB 1162 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1221
OY 321 ThrAlaAlaGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 340
DB 1222 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1281

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OY 341 MetGluGluLeuGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 360
DB 1283 CGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1341
OY 361 MetSerAlaAlaThrValThrPheGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 380
DB 1342 ACAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1401
OY 381 ThrThrValIleIleLeuSerProValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 400
DB 1402 ACCAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 461
OY 401 ThrIleGluIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 420
DB 1462 ACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
OY 421 LeuIleGluIleValAlaLeuValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 440
DB 1522 CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1581
OY 441 LeuAlaLysSerSerValProIleIleThrIleGluIleGlyIleGlyIleGlyIleGlyIle 460
DB 1582 TGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1641
OY 461 GlyIleAlaAlaCysIleAlaIleThrIleGluIleGlyIleGlyIleGlyIleGlyIleGly 480
DB 1642 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1701
OY 481 ArgProGlySerGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 500
DB 1702 CGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1761
OY 501 GluAlaValIleHisPheIleCysSerIleValProIleValProIleValProIleValPro 516
DB 1762 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809

RESULT 2
; Sequence 1: Application 05/10096960
; Publication No. US2002013325A1
; GENBANK accession: J05819
; TITLE: INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: C00015516V
; CURRENT APPLICATION NUMBER: US/10/096,960
; CURRENT FILING DATE: 2002-03-14
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO: 1
; SEQ ID NO: 2
; SEQ ID NO: 3
; SEQ ID NO: 4
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-096-960-1

Alignment Scores:
Score: 236-245
Length: 2061
Percent Similarity: 79.86%
Matches: 434
Best Local Similarity: 74.70%
Mismatches: 86
Identical: 81
Dels: 13
Gaps: 5

US-09-820-790b-2 (1-516) x US-10-096-960-1 (1-2061)
OY 1 MetAlaThrValThrValThyCysThrArgPheThrAspGluValGlyLeuValGlyAspLeu 20
DB 113 ATGCCACAGAGTGTGTGATGACGCTCCGCTCCGACGAGGATCCATCTGACGAGGAT 172
OY 21 GlyValGlyAlaPheSerValAlaArgCysValGlyValGlyValGlyValGlyValGlyValGly 190

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455 ProLysValHisValIleGlyValAspAlaGlyIleAlaAlaIleLeuLeuThrIn 474
 1249 CCGCATCATCTGTAAGGAGTATGAGCGGCTGATGATGATATATAGCTCACAG 1308
 475 TactLeuGlyGlyGlyProArgHisSerGlnGlnHisValIlePhe 494
 1309 TACATGATGGAGTGGATGCGAAGGAGATGATGAGAGAGTCTGTGTGGAC 1368
 495 ArgArgLeuGlyValGlyGlnGlnValHisLeuPheLeuGlyGlyValHisLeu 514
 1365 CCGAGGATGGATGAGTGGAGTGGATGATGATGATGATGATGATGATGATGAT 1428
 515 LeuGln 516
 1429 ATGAG 1434

RESULT 6
 US-10-393-892-1
 : Sequence 1, Application US/103982
 : Sequence 2, Application US/103982
 : GENERAL INFORMATION:
 : APPLICANT: WMS; TEXIN
 : PROJECT: CANCER DIAGNOSTICS
 : FILE REFERENCE: CDS 247 US NP
 : CURRENT APPLICATION NUMBER: US/10/393-892
 : CURRENT FILING DATE: 2002-09-21
 : PRIOR FILING DATE: 2002-09-29
 : NUMBER OF SEQ ID NOS: 49
 : SEQ ID NO 1 Patent version 3.1
 : LENGTH: 1500
 : TYPE: DNA
 : SPECIES: human
 : US-10-393-892-1

Alignment Scores:
 Pct: 80.1
 Score: 396
 Percent Similarity: 78.784
 Percent Identity: 78.784
 Query Match: 60
 Gaps: 3
 Length: 1500

US-09-820-790b-2 (1-516) x US-10-393-892-1 (1-1500)
 QY 1 MetAlaThrValThrCysThrArgPheThrAspGlyThrGlnLeuValAspIle 20
 DB 1 AAGGCTTTCGACACACATGCGACACATTCGCGGACGACGATTCGATTTTGGAGGCTT 60
 QY 21 GlyIleValAlaPheSerValValArgGlyCysValLysLeuGlyHisLeuVal 40
 DB 61 GGAGAGGGGAGATCTGATGCGAGAGATGATGAGGATGATGAGGATGATGAGGAT 120
 QY 41 AlaAlaGlyIleLeuThrGlyCysGlnSerAlaArgAspIleLysLeuGly 60
 DB 121 GTGCGCAAAATATACACACCAAAAGGCTTCTGTAGGATCTAGAGATGAGAGA 180
 QY 61 GluAlaValHisCysArgGlnGlnHisSerValHisLeuPheLeuGlyHisLeu 80
 DB 181 GAGCTGAGATGCTGGCTGTTTGAAGCACTTATATGTGGGATTCATGATAGATCA 240
 QY 81 SerGlnGlyGlyPheValThrValPheArgGlyValHisCysGlyValHisLeu 100
 DB 241 TCAGAAAGGGGCTTCTACTACTGCTGTGATGATGATGATGATGATGATGATGAT 300
 QY 101 AspIleValAlaGlyGlyValThrGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 DB 301 GAGATGCGCAGAGATACTGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 121 LeuValAlaLeuHisValCysHisGlnLeuGlyValHisLeuPheLeuValPhe 140

361 CTGAAATGTGTTATCATCTGCACTTAATGAGCATAGTTCACAGGAGCATGAGCTGAG 420
 QY 141 ArgLeuLeuLeuAlaSerValCysGlyGlyValAlaThrValThrLeuAlaHisPheGly 160
 DB 141 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 480
 142 ATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 480
 QY 161 AlaThrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 180
 DB 161 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 540
 162 ATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 540
 QY 181 LeuSerProGlyValLeuAlaGlyValAlaValCysGlyValPheValLysLeuPheVal 200
 DB 181 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 260
 201 CTTTCTTCGAGATTTTCTGTAAGATCTTATCTTGAAGGCTGCTGATGATTTGGGCAAGT 220
 QY 201 GlyValIleLeuValThrIleLeuLeuAlaValCysGlyProPheThrPaspGlyHisLeu 240
 DB 201 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 300
 221 LysLeuValGlyGlnIleValAlaValAlaValAspPheProSerProLysPheThr 240
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 381 ThrThrValIleHisAsnProValAspGlyIleGlySerSerSerSerAlaAsnThr 400
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 DB 434 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 434
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 435 ThrThrPheGlyHisLeuAlaAlaGlyHisSerGlyProLeuThrThrThrThrThrThr 454
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GenCore version 5.1.6

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ON protein - protein search, using sw model.

Run on: October 10, 2003, 04:14:34 ; Search time 83 Seconds

(Without alignments)
986,782 Million cell updates/sec

Title: US-09-820-790b-2

Perfect score: 2715

Sequence: 1 KATVVCITRFDRFQVET.....DEKNWVHSCAPAFVQLQ 516

Scoring table: BLASTN62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 138726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Maximum Match 94

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

- 1: /SIDSL/seqdata/geneseq-emb/AA180.DAT.*
- 2: /SIDSL/seqdata/geneseq-emb/AA181.DAT.*
- 3: /SIDSL/seqdata/geneseq-emb/AA182.DAT.*
- 4: /SIDSL/seqdata/geneseq-emb/AA183.DAT.*
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- 19: /SIDSL/seqdata/geneseq-emb/AA198.DAT.*
- 20: /SIDSL/seqdata/geneseq-emb/AA199.DAT.*
- 21: /SIDSL/seqdata/geneseq-emb/AA200.DAT.*
- 22: /SIDSL/seqdata/geneseq-emb/AA201.DAT.*
- 23: /SIDSL/seqdata/geneseq-emb/AA202.DAT.*
- 24: /SIDSL/seqdata/geneseq-emb/AA203.DAT.*

Pred. No. is the number of results predicted by chance to have a
score at least as high as the observed score printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	ID	Description
1	2715	100.0	516_24	AA30198.....
2	2692	99.2	542_23	AA30198
3	2476.5	91.2	641_21	AA56791
4	2476.5	91.2	641_21	AA56791
5	2244	85.1	598_23	AA36276
6	2230	82.1	525_22	AA72441
7	2230	82.1	525_22	AA72441
8	2225.3	82.0	565_24	AA56793
9	2225.3	82.0	565_24	AA56793

10	2222	81.8	518_22	AAK7457	Human protein S80
11	2070	76.2	499_22	AAU03512	Human protein kinase
12	2069	76.2	500_22	AAU03512	Human protein kinase
13	2065	76.2	605_22	AA314826	Novel human diaph
14	1872	69.0	493_22	AA365515	broscophila melanog
15	1872	69.0	493_22	AA365515	broscophila melanog
16	1872	69.0	493_22	AA365515	broscophila melanog
17	1775.5	65.4	461_24	AA394055	Human protein kinase
18	1544.5	56.9	372_22	AAU87348	Human central nerv
19	1405	47.7	364_20	AA394050	rat protein kinase
20	1395	47.7	364_20	AA394050	rat protein kinase
21	1294	47.7	264_20	AA743913	Novel human kinase
22	1270.5	46.8	469_24	AA394084	Human protein kinase
23	1138	41.3	282_21	AA365515	broscophila melanog
24	1138	41.3	282_21	AA365515	broscophila melanog
25	860.5	31.7	236_22	AA30751	Novel human diaph
26	860.5	31.7	236_22	AA30751	Novel human diaph
27	850	31.7	500_22	AA365515	broscophila melanog
28	850	31.7	500_22	AA365515	broscophila melanog
29	619.5	22.8	284_22	AA315059	Human nervous syst
30	619.5	22.8	284_22	AA315059	Human nervous syst
31	616.5	22.7	335_22	AA365515	broscophila melanog
32	616.5	22.7	335_22	AA365515	broscophila melanog
33	616.5	22.7	385_22	AA365515	broscophila melanog
34	616.5	22.7	385_22	AA365515	broscophila melanog
35	613.5	22.6	357_22	AA314768	Human kinase (PKIN
36	610.5	22.5	450_22	AA365515	broscophila melanog
37	610.5	22.5	450_22	AA365515	broscophila melanog
38	607	22.4	356_22	AA365515	broscophila melanog
39	605.5	22.3	405_22	AA365515	broscophila melanog
40	593	21.8	385_22	AA365515	broscophila melanog
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44	584.5	21.5	460_23	AA365515	broscophila melanog
45	584.5	21.5	460_23	AA365515	broscophila melanog

ALIGNMENTS

Result 1
AA30198
ID AA30198 standard: Protein: 516 AA.

XX AA30198;

IT 24-FEB-2003 (first entry)

XX Human kinase protein.

XX Human calcium/calmodulin-dependent protein kinase; immune response;

XX growth factor receptor; gene cluster; gene cluster; gene cluster;

XX growth disorder; developmental disorder; chromosome 7.

XX Homo sapiens.

XX Key

FT Modified-site

FT Region

FT /note= "Tyrosine kinase phosphorylation site"

FT /note= "Protein kinase ATP-binding region signature"

FT Modified-site

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site

FT /note= "Protein kinase C phosphorylation site"

FT Modified-site

FT /note= "GMP and GTP-dependent protein kinase phosphorylation site"

FT Modified-site

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site

FT /note= "Protein kinase C phosphorylation site"

XX	PD	12-SEP-2002.	
XX	XX	28-FEB-2002; 2002W0-EP021495.	
XX	XX	01-MAR-2001; 2001B0-010562.	
XX	FR	(LON) - LION BIOENGINEER, A.	
XX	PI	Albers M, Ellmanger S, Loser E, Koegl M:	
XX	PI	WPLT-2002-713453/77.	
XX	OR	N-DSB; AB223378.	
XX	XX	New cofactors of estrogen receptor alpha, designated as CTF1, CPT1,	
XX	XX	CTF2, CTF3, CTF4, CTF5, CTF6, CTF7, CTF8, CTF9, CTF10, CTF11,	
XX	XX	CTF12, CTF13, CTF14, CTF15, CTF16, CTF17, CTF18, CTF19, CTF20,	
XX	XX	CTF21, CTF22, CTF23, CTF24, CTF25, CTF26, CTF27, CTF28, CTF29,	
XX	XX	CTF30, CTF31, CTF32, CTF33, CTF34, CTF35, CTF36, CTF37, CTF38,	
XX	XX	CTF39, CTF40, CTF41, CTF42, CTF43, CTF44, CTF45, CTF46, CTF47,	
XX	XX	CTF48, CTF49, CTF50, CTF51, CTF52, CTF53, CTF54, CTF55, CTF56,	
XX	XX	CTF57, CTF58, CTF59, CTF60, CTF61, CTF62, CTF63, CTF64, CTF65,	
XX	XX	CTF66, CTF67, CTF68, CTF69, CTF70, CTF71, CTF72, CTF73, CTF74,	
XX	XX	CTF75, CTF76, CTF77, CTF78, CTF79, CTF80, CTF81, CTF82, CTF83,	
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XX	XX	CTF406, CTF407, CTF408, CTF409, CTF410, CTF411, CTF412, CTF413,	
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DB	481	HHV8VIRUSGACACATATCTCTTIDGGGRTSGSRETRVMBRGGQVNFVFCSCAPAF	540
QY	515	LO 516	
DB	541	LO 542	
RESULT 3			
ID	AN68791	standard; Protein: 641 AA.	
AC	AN68791;		
XX	16-MAY-2000	(first entry)	
XX	XX		
XX	XX		
XX	XX		
XX	XX	Amino acid sequence of a human phosphorylation effector PRSP-23.	
XX	XX	Human: phosphorylation effector; PRSP; proliferative disorder;	
XX	XX	immune disorder; neuronal disorder.	
XX	XX		
XX	XX	Bomo sapiens.	
Key	Location/Qualifiers		
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FT	1	note="potential phosphorylation site"	
FT	36	note="protein kinase signature sequence"	
FT	20..43		
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FT	94	note="potential phosphorylation site"	
FT	1	note="potential phosphorylation site"	
FT	119..156	note="ATP-binding site"	
FT	1	note="protein kinase signature sequence"	
FT	131..214	note="ATP-binding site"	
FT	252	note="protein kinase signature sequence"	
FT	1	note="potential phosphorylation site"	
FT	313	note="potential glycosylation site"	
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FT	422	note="potential phosphorylation site"	
FT	431	note="potential phosphorylation site"	

PT Nucleic acid molecules encoding calcium/calmodulin-dependent protein kinases, useful for preventing diagnosing and treating e.g. cancers,

claim 1: Fig 2A; 85pp; English.

[illegible]

Seq	Sequence	565 AA;	Query Match 94.7%	Score 2225.5	DB 23;	Length 565;
			Similarity	Pos. No.	Pos. No.	
			Matches	34;	Mismatches 36;	Indels 81; Gaps 5;
QY	1	MATTCTFTFTFDTQVLELGGAFQPVKQVQKQVETAKINKLSEADHQLKRL	60			
QY	1	MATTCTFTFTFDTQVLELGGAFQPVKQVQKQVETAKINKLSEADHQLKRL	60			
QY	61	EAICRLKILKLVHDSISEELPVPFLDTGLVGLSEFVAVSEYSEADHQLKRL	120			
QY	61	EAICRLKILKLVHDSISEELPVPFLDTGLVGLSEFVAVSEYSEADHQLKRL	120			
QY	121	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	180			
QY	121	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	180			
QY	181	LSPTFLKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	240			
QY	181	LSPTFLKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	240			
QY	241	VTPFAKILKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	300			
QY	241	VTPFAKILKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	300			
QY	301	KGAILTVKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	359			
QY	301	KGAILTVKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	359			
QY	360	KNSAANTSPGTLFPAAPQVTVHINVDIKESDGAATILEDEKAA	409			
QY	360	KNSAANTSPGTLFPAAPQVTVHINVDIKESDGAATILEDEKAA	409			
QY	409	VPEKILKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	468			
QY	409	VPEKILKLVKGVKQVETAKINKLSEADHQLKRLVQIGAGATQVSPFMT	468			
QY	469	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	528			
QY	469	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	528			
QY	529	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	588			
QY	529	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	588			
QY	589	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	648			
QY	589	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	648			
QY	649	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	708			
QY	649	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	708			
QY	709	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	768			
QY	709	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	768			
QY	769	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	828			
QY	769	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	828			
QY	829	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	888			
QY	829	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	888			
QY	889	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	948			
QY	889	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	948			
QY	949	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1008			
QY	949	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1008			
QY	1009	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1068			
QY	1009	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1068			
QY	1069	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1128			
QY	1069	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1128			
QY	1129	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1188			
QY	1129	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1188			
QY	1189	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1248			
QY	1189	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1248			
QY	1249	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1308			
QY	1249	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1308			
QY	1309	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1368			
QY	1309	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1368			
QY	1369	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1428			
QY	1369	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1428			
QY	1429	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1488			
QY	1429	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1488			
QY	1489	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1548			
QY	1489	LEAVLKHGTVGVHRELKELKLASKGKAVKLAGLTVQGVQAWGAGTFT	1548			
QY						

RESULT 9

ABG75873

ID YK

XX The invention relates to polypeptides (AM53456-AM53457) and the
 CC nucleic acids encoding them, to methods for producing cytokines to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polypeptides and nucleic acids are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides are useful in the treatment of
 CC e.g. stem cell growth factor activity, hematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Records for 580 ID NO 2110 (AM532581), 2111 (AM532582) and 3666
 CC (AM532583) were missing at the time of publication.
 CC

XX Sequence 518 AA:

Query Match 81.84; Score 222; DB 22; Length 518;
 Best Local Similarity 73.04; Pred. No. 2.9e-204;
 Matches 425; Conservative 31; Mismatches 57; Indels 52; Gaps 4;
 QY 1 MATVTCRFEDTVDLDEIGKASVSRVCLTQGHFAAKITKLSARHOKLER 60
 XX
 XX 1 MATVATCTVDLQFELGKASVSRVCLTQGHFAAKITKLSARHOKLER 60
 DB
 QY 61 EARCILLKSHVILHSDISISEBPTFLVPLVGGELFEDVARTSEADNSICDQI 120
 XX
 QY 61 EARCILLKSHVILHSDISISEBPTFLVPLVGGELFEDVARTSEADNSICDQI 120
 DB
 QY 121 LEAVLKHCHQVWHEELKFNLLASKGAAVLAFLGLAVDQDQAGFAGTST 180
 XX
 QY 121 LEAVLKHCHQVWHEELKFNLLASKGAAVLAFLGLAVDQDQAGFAGTST 180
 DB
 QY 181 LSPFLKATKNGKVDWACVYLILVGVPPFDVGHLYLQTKAGADPFSBPT 240
 XX
 QY 181 LSPFLKATKNGKVDWACVYLILVGVPPFDVGHLYLQTKAGADPFSBPT 240
 DB
 QY 241 VTFPANELNQLMFINPAIRLAEAKHPWQCVASMERQSTVLEKLENAEEL 300
 XX
 QY 241 VTFPANELNQLMFINPAIRLAEAKHPWQCVASMERQSTVLEKLENAEEL 300
 DB
 QY 301 KGAULTMLNMFSGVQGTAPATNGVASTCTNGLVSEANSLANKADLQWPTNPT 359
 XX
 QY 301 KGAULTMLNMFSGVQGTAPATNGVASTCTNGLVSEANSLANKADLQWPTNPT 359
 DB
 QY 360 KKAASATSGTLPALALPQTVLHNVGLIKESDANTTIEEERAKRQIKTE 419
 XX
 QY 336 KNSVSPQAPLQFAPQVETQVTHMARGISRGSTSCFTTDEGLAKVQIKTE 395
 DB
 QY 420 QLEAVNGQFAPAYLA- - - - -TFENLAKNSKTEHTIL 453
 XX
 QY 396 QLEAVNGQFAPAYLA- - - - -TFENLAKNSKTEHTIL 455
 DB
 QY 454 NRPVETDEACATYATFELQIDGQRFQSGSEPTVWRHDSKQNVHFCSSAPA 513
 XX
 QY 456 NRPVETDEACATYATFELQIDGQRFQSGSEPTVWRHDSKQNVHFCSSAPA 515
 DB
 QY 514 PLQ 516
 XX
 QY 516 PLQ 518
 DB

RESULT 11

AMU03512

ID AMU03512 standard; Protein: 499 AA.

XX AMU03512

XX AMU03512;

DT 12-SEP-2001 (first entry)

XX Human protein kinase 12.

XX

KW Human; protein kinase: PK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW infectious disease; inflammatory disorder; infectious disease;
 KW reproductive disorder.

XX Homo sapiens.

XX W0200138509-A2.

PN 31-MAY-2001.

XX 22-MAY-2000; 2000R00-US32085.

XX 24-NOV-1999; 5908-0167482.

XX (SDG-) SUGEN INC.

PA Ploman GD, White D, Manning G, Subramaniam S, Martleson R,

PI Flanagan P, Clary D;

XX WPI: 2001-319850/76.

XX M-FSIR; AAS06712.

XX Nucleic acids encoding human kinase polypeptides, useful for preventing
 XX cancer and various diseases, and for preventing viral, cellular and
 XX neuronal-associated diseases, and microbial infections -
 XX

Claim 7: Figure 2: 43pp; English.

CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The
 CC novel protein kinases have been identified as members of the tyrosine
 CC kinase family. The kinases are useful for preventing and treating
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC cancer, hematopoietic disorders, hematopoietic disorders, heart
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC cancer (e.g. leukemias), hematopoietic disorders (e.g. myelodysplastic
 CC disease), inflammatory disorders (e.g. asthma), infectious
 CC diseases (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additonal polypeptides encoding protein kinases may be
 CC identified by screening the human genome for novel protein kinases.
 CC The protein kinase polypeptides may be used as antigens in the production
 CC of antibodies against the protein kinases and in assays to identify
 CC modulators of protein kinase expression and activity.

XX Sequence 499 AA:

Query Match 74.28; Score 2070; DB 22; Length 499;
 Best Local Similarity 73.18; Pred. No. 1.1e-189;
 Matches 356; Conservative 31; Mismatches 25; Indels 90; Gaps 3;
 QY 1 MATVTCRFEDTVDLDEIGKASVSRVCLTQGHFAAKITKLSARHOKLER 60
 XX
 XX 1 MATVTCRFEDTVDLDEIGKASVSRVCLTQGHFAAKITKLSARHOKLER 60
 DB
 QY 61 EARCILLKSHVILHSDISISEBPTFLVPLVGGELFEDVARTSEADNSICDQI 120
 XX
 QY 61 EARCILLKSHVILHSDISISEBPTFLVPLVGGELFEDVARTSEADNSICDQI 120
 DB
 QY 121 LEAVLKHCHQVWHEELKFNLLASKGAAVLAFLGLAVDQDQAGFAGTST 180
 XX
 QY 121 LEAVLKHCHQVWHEELKFNLLASKGAAVLAFLGLAVDQDQAGFAGTST 180
 DB
 QY 181 LSPFLKATKNGKVDWACVYLILVGVPPFDVGHLYLQTKAGADPFSBPT 240
 XX
 QY 181 LSPFLKATKNGKVDWACVYLILVGVPPFDVGHLYLQTKAGADPFSBPT 240
 DB
 QY 241 VTFPANELNQLMFINPAIRLAEAKHPWQCVASMERQSTVLEKLENAEEL 300
 XX
 QY 241 VTFPANELNQLMFINPAIRLAEAKHPWQCVASMERQSTVLEKLENAEEL 300
 DB

b	417	PHEWLMVDDACINATLRLQYMDGDSMTKTSSEETPVHNRGRKQKVHFSSSPVP	476
y	513	IQ	516
b	477	IK	78
<hr/>			
RESULTS 13			
ID	AB016026	standard; Protein: 605 AA.	
CD	AB016026		
NC	AB016026;		
CX	13-FEB-2002	(first entry)	
TX	Novel human disintegrin protein t46B17.		
SX	human; chromosome mapping; gene mapping; gene therapy; forensic;		
KX	food supplement; medical imaging; diagnostic; genetic disorders.		
WX	WO2001/57667-A2.		
MX	HO2001/57667-A2.		
DX	11-OCT-2004.		
FX	30-MAR-2004; 2001MO-US98631.		
GX	31-MAR-2000; 2000US US040217.		
HX	23-AUG-2000; 2000SG US043167.		
JX	(HSEP)- HYSEQ INC.		
KX	Tzannac RT, Liu C, Tang YF;		
LX	WPI; 2001-639362/73.		
MX	N-PSDB; AAS84013.		
NX	New isolated polynucleotide and encoded polypeptides, useful in		
OX	diagnostics, forensics, gene mapping identification of mutations		
PO	for genetic disorders or other traits and to assess		
PT	diversity		
QU	Citation 20; SEQ ID NO 4785; 10pp; English.		
RX	The invention relates to isolated polynucleotide (I) and		
SC	polypeptide (II) sequences. (i) is useful as hybridization probes,		
TC	gene mapping, and in recombinant production of (II). The		
UC	polynucleotides are also used in diagnostics as expressed sequence tags		
VX	for identifying expressed genes. (I) is useful in gene therapy techniques		
WC	for identifying expressed genes. (I) is useful in gene therapy techniques		
XZ	(II). (II) is useful for generating antibodies against it, detecting or		
YC	quantitating a polypeptide in tissue, as molecular weight markers and as		
ZC	a food supplement. (II) and its binding partners are useful in medical		
CC	diagnoses involving aberrant protein expression or biological activity.		
DC	The polypeptide and polynucleotide sequences have applications in		
EC	diagnostics, forensics, gene mapping, identification of mutations		
FC	for genetic disorders or other traits and to assess diversity		
GC	and to produce other types of data and products dependent on DNA and		
HC	amino acid sequences. Abm00010-tac10197 represent novel human		
IC	uronic acid sequences. Abm00010-tac10197 represent novel human		
JC	wound healing factors. This patent did not appear in the printed		
KC	schematic diagram, but was obtained in electronic format directly from WIPO		
LC	at ftp://pat.int/pub/published_pat_sequences.		
MC	Sequence 605 AA;		
NC			
<hr/>			
Query Match	76.1%	Score 2667;	Ds 22; Length 605;
Similarity	35.7%	Positives 18/25;	Indels 19;
Conservative	32.0%	Swatches 25;	Indels 19;
Gap	35.0%	Swatches 25;	Indels 19;

Fri Oct 10 17:19:10 2003

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Page 15

DD 360 TQULIEAINSDFQTKICDPLHANTPEBALGNLVEGLDFHRTTFENYLGKXALNTT 419
QY 452 ILAPRNVYIGEDAGIAIYELQYIDQOPRFSUSESTRWHRDCKWQWAPRUGA 510
DD 420 ILAPRNVLLREAGIAVILZOTLWQGHAFQSESTRWHRDCKWQWAPRUGA 478

Search completed: October 10, 2003, 08:08:03
Job time : 87 secs


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121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 421 LITAVNNDQFVFA 454
Db 421 LITAVNNDQFVFAKICDGLSPFPAALGNVQDGFHFTFFNLANSKSPHTITLIN 480
Db 421 LITAVNNDQFVFAKICDGLSPFPAALGNVQDGFHFTFFNLANSKSPHTITLIN 480
Db 455 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 514
Db 455 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 514
Db 481 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 540
Db 515 LQ 516
Db 541 LQ 542

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RESULT 2

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C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1998 (sequence_revision 30-Jun-1998 #ext_change 11-Jun-1999
R:Bennett, M.K.; Kennedy, M.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1794-1798, 1987
A:Reference number: A26464; MIMD:8775561; PMID:3470758
A:Accession: A26464
A:Molecule type: mRNA
A:Cross-references: GI:65112; NID:q206170; PIR:AAAI865.1; PID:q206171
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
A:Note: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
C:Superfamily: G2a/calmodulin-dependent protein kinase II; protein kinase homology
P:12-27/Domain: protein kinase homology <XIN>
P:12-27/Region: protein kinase ATP-binding motif
P:20-26/Region: calmodulin binding status predicted
P:43-51/Region: calmodulin binding status predicted
P:287/Binding site: Phosphate (Thr) (covalent) (by autophosphorylation) status predicted
Query Match Similarity 98.3%; Score 3659; DB 3; Length 542;
Best Local Similarity 94.3%; Pred. No. 3.9e-112;
Matches 51; Conservative 2; Mismatches 3; Indels 26; Gaps 1;

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Db 1 MATVTCFTEYDQTEVDGGSVYHRRQVCLCTHFAKTIINFLASAROKLER 60
Db 61 EATLCRLKSNVYILGDSISEPHITVFDVQGLFEDVAVRYTSEADSCIQI 120
Db 61 EATLCRLKSNVYILGDSISEPHITVFDVQGLFEDVAVRYTSEADSCIQI 120
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180

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181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 241 VYFPAELINQMLTINAKETIATBALAKHPWQGSVYASNGHGFVCLKFNAREKL 300
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 301 KQALITLMTATFNSVGGTATVATNASTGTGMLVQASLAKKQDKEQNSTK 360
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 361 NSNATFPGTTPPAALPEQTVTVINPVQVIGKSSDQSNITTEDAKAKQETITRQ 420
Db 421 LITAVNNDQFVFA 454
Db 421 LITAVNNDQFVFAKICDGLSPFPAALGNVQDGFHFTFFNLANSKSPHTITLIN 480
Db 421 LITAVNNDQFVFAKICDGLSPFPAALGNVQDGFHFTFFNLANSKSPHTITLIN 480
Db 455 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 514
Db 455 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 514
Db 481 PHRTVIGDQACIATITLQYDQGGPFGSSTVYHRRQDKNVHRCGSAVP 540
Db 515 LQ 516
Db 541 LQ 542

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RESULT 3

```

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1998 (sequence_revision 30-Jun-1998 #ext_change 18-Jun-1999
R:Bennett, M.K.; Kennedy, M.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1794-1798, 1987
A:Reference number: A26464; MIMD:8775561; PMID:3470758
A:Accession: A26464
A:Molecule type: mRNA
A:Cross-references: GI:65112; NID:q206170; PIR:AAAI865.1; PID:q206171
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
A:Note: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
C:Superfamily: G2a/calmodulin-dependent protein kinase II; protein kinase homology
P:12-27/Domain: protein kinase homology <XIN>
P:12-27/Region: protein kinase ATP-binding motif
P:20-26/Region: calmodulin binding status predicted
P:43-51/Region: calmodulin binding status predicted
P:287/Binding site: Phosphate (Thr) (covalent) (by autophosphorylation) status predicted
Query Match Similarity 97.8%; Score 3701.5; DB 2; Length 559;
Best Local Similarity 75.0%; Pred. No. 5.4e-99;
Matches 47; Conservative 2; Mismatches 4; Indels 13; Gaps 4;

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Db 1 MATVTCFTEYDQTEVDGGSVYHRRQVCLCTHFAKTIINFLASAROKLER 60
Db 61 EATLCRLKSNVYILGDSISEPHITVFDVQGLFEDVAVRYTSEADSCIQI 120
Db 61 EATLCRLKSNVYILGDSISEPHITVFDVQGLFEDVAVRYTSEADSCIQI 120
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 121 LEAVLCHONGVHEDLAKPENCILASCKGAAGVLAFLAVQDQAMFGAGTGY 180
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240
Db 181 LSPVTLREAGVGVNDVNAQGVYLLIVLVYPPFMDQDRLVQYQAGNDFPSPMOT 240

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A:Map position: 4	100/3; 124/3; 185/3; 217/3; 218/3; 286/3; 302/3; 342/3; 375/3; 413/3
C:Superfamily: Q22/calmodulin-dependent protein kinase II; protein kinase homology	
Query Match	58.66; Score 1590.7; DD 2; Length 547;
Query Similarity	64; Mismatches 103; Indels 59; Gaps 9;
Matches 312; Conservative 64; Mismatches 103; Indels 59; Gaps 9;	
QY 18	EDIGAGNSVRCVKLTCTHRAKANTIKRQANQKRWKNSAFQKLRKSNVRLR 77
DB 4	QOINSGASVSRVYHTLGFPAKTIKFKLGGADQCKLERAKCRKQDPIVRLR 63
QY 76	DSISREPTPLVPLVQDELVDVARYETSEADASNIQQLLEAFKRWKVVHDL 137
DB 6	KSIOESRFLVPLVQDELVDVARYETSEADASNIQQLLEAFKRWKVVHDL 123
QY 136	KPKNLLASCKGKAVLAQPLATVQDQCAWPFQAGTSPVSPVLRKATKGVPI 197
DB 64	DSIOESRFLVPLVQDELVDVARYETSEADASNIQQLLEAFKRWKVVHDL 123
QY 138	KPKNLLASCKGKAVLAQPLATVQDQCAWPFQAGTSPVSPVLRKATKGVPI 197
DB 124	KPKNLLASCKGKAVLAQPLATVQDQCAWPFQAGTSPVSPVLRKATKGVPI 192
QY 194	WACQVILYLLVTPFQDEDEHKLQIKAGATQSPFPMVTPPAKLNKQLTNP 257
DB 183	WACQVILYLLVTPFQDEDEHKLQIKAGATQSPFPMVTPPAKLNKQLTNP 242
QY 258	AKRTIAHAKLHFWQRTSVASMHQRTYECLEKFNARKIGALITMLATNFG 317
DB 243	KRLTNGQALVYFENKRSKALSRDQVQLAFKAPARAKALANVATNSQVL 302
QY 338	ROTAPAKMTAAQDTT----- 334
DB 303	R-TSUSTQSVASSGTTTHASQVAGTSQSPPAKAYVPWLLFNKTFPKVHPPT 340
QY 334	-----KLLNKAD----- 341
DB 361	RYTSVSKSKLPTLLFVCPHSFSLHLLDNTFNINLYHVFYFKNSHFAAS 420
QY 342	-----GKYEQT----- 408
DB 421	SHRSSTKCANALVTRSSPSIRKTAQVHNSRWKVSANALQALPVIVW 480
QY 379	PQTVY----- 408
DB 481	VATGASSYTNLSASTSDGLNKLKKIQPPTTSKSSSSQ-TIDNSEEQSG 539
QY 409	-----AKCKELIVTETQLTANNQHPKAY 434
DB 540	LAHNTVYAGATGVSSSSNSTASKSSSTINAGKQDVTATQTLAASQAPFTT 599
QY 433	-----FTYENLLANSKP----- 488
DB 600	RLCQFATCFPEALONLEIHFPHFTD---GNKQVYHTFETQLTANNQHPKAY 656
QY 469	YTRLDYTDGQRPFTSCSEPTFVHWRHQRDQVWVFHFGSAP 511
DB 657	YKLTQFLDRHGAHTQSGSRVSKGQGWVYVHSTQPT 699

Search completed: October 10, 2003, 08:11:31
Job time: 48 secs

RESULT 15

T23516	cytohectol protein, K118L,lc
A:Accession: T23516	Genbank accession: T23516
C:Date: 15-Oct-1999	Sequence revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T23516	
A:Reference number: 219771	submitted to the EMBL Data Library, March 1996
A:Accession: T23516	
A:Molecule type: DNA	transcribed from QY/DBGL/DBJ
A:Residues: 1-708 	
A:Cross-references: BMRB:770279; RIKEN Q6A9144.1; GSPDB:G000022; CESP:K118L.lc	
C:Genetics:	
A:Gene: CESP:K118L.lc	
A:Position: 8/3	
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol	
Query Match	55.38; Score 1503; DD 2; Length 708;
Query Similarity	64; Mismatches 101; Indels 216; Gaps 12;
Matches 324; Conservative 64; Mismatches 101; Indels 216; Gaps 12;	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

No.	Query	Score	Match	Length	DB	ID	Description
1	2522	98.4	542	1	KCDB_MOUSE	P86522	mus musculus
2	2659	98.3	542	1	KCDB_MOUSE	P88413	rattus norv
3	2611	96.5	554	1	KCDB_HUMAN	O13154	homo sapien
4	2215	91.6	569	1	KCDB_MOUSE	O31496	mus musculus
5	2815	81.6	569	1	KCDB_MOUSE	O31419	mus musculus
6	2077	80.2	538	1	KCDB_RAT	P57911	rattus norv
7	2319	74.1	488	1	KCDB_MOUSE	P11275	rattus norv
8	2019	74.1	488	1	KCDB_HUMAN	Q9UG77	homo sapien
9	2085	74.0	478	1	KCDB_HUMAN	P11275	mus musculus
10	1915	69.5	428	1	KCDB_MOUSE	O14936	homo sapien
11	1945	67.9	428	1	KCDB_MOUSE	O14936	homo sapien
12	1736	37.1	906	1	GSF_HUMAN	P08710	homo sapien
13	725	36.7	906	1	GSF_RAT	O62813	rattus norv
14	612	36.7	906	1	GSF_MOUSE	O62813	rattus norv
15	633	35.3	844	1	KCDB_RAT	P11234	rattus norv
16	622	22.9	459	1	KCDB_MOUSE	P88414	mus musculus
17	616	22.7	459	1	KCDB_HUMAN	O65656	homo sapien
18	591	21.8	459	1	KCDB_MOUSE	O65656	homo sapien
19	591	21.8	374	1	KCDB_RAT	O63450	rattus norv
20	587	21.6	374	1	KCDB_MOUSE	O63450	rattus norv
21	587	21.6	374	1	KCDB_MOUSE	O63450	rattus norv
22	583	21.5	433	1	KCDB_RAT	O68755	rattus norv
23	583	21.5	736	1	KCDB_MOUSE	O68755	rattus norv
24	577	21.1	736	1	KCDB_MOUSE	O68755	rattus norv
25	577	21.1	736	1	KCDB_MOUSE	O68755	rattus norv
26	568	20.6	508	1	KCDB_HUMAN	O31496	mus musculus
27	568	20.6	531	1	KCDB_MOUSE	O31496	mus musculus
28	568	20.6	508	1	KCDB_HUMAN	P58813	glycine max
29	549	20.2	466	1	KCDB_HUMAN	P58813	glycine max
30	549	20.2	466	1	KCDB_HUMAN	P58813	glycine max
31	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
32	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
33	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
34	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
35	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
36	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
37	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
38	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
39	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
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41	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
42	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
43	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
44	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
45	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
46	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
47	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
48	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
49	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
50	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
51	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
52	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
53	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
54	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
55	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
56	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
57	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
58	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
59	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
60	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
61	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
62	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
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64	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
65	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
66	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
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70	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
71	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
72	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
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74	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
75	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
76	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
77	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
78	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
79	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
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81	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
82	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
83	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
84	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
85	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
86	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
87	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
88	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
89	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
90	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
91	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
92	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
93	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
94	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
95	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
96	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
97	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
98	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
99	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max
100	547	20.2	466	1	KCDB_HUMAN	P58813	glycine max

AT-TCHMPPTS

RESULT 1
ID KCCB_MOUSE
STANDARD: PRT: 542 A9

AC P28652;
DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase

(EC 2.7.1.123) (CaM-kinase II β beta chain) (CaM-K-II beta subunit).

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eumammalia; Theria; Eutheria; Rodentia; Muridae; Murinae; Murini; Mus.

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi;
OX NCBI_TaxID=10090;
      [1]
      GEN

```

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      SEQUENCE FROM N.A.
      STRAIN=BALB/c; TISSUE=Brain;
      MEDLINE=92334366; PubMed=1321343;

```

Karls U., Mueller U., Gilbert D.J., Copeland
Harbers K.:

Structure, expression, and chromosome location of the human β -subunit of brain-specific Ca^{2+} /calmodulin-dependent kinase II identified by transgene integration

mouse mutant,";
Mol. Cell. Biol. 12:3644-3652(1992).
-1- FUNCTION: THIS KINASE MAY PLAY A ROLE IN

- CATALYTIC ACTIVITY: ATP + protein - ADP
- ENZYME REGULATION: AUTOPHOSPHORYLATION

- I - SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS AND DELTA.

CC -!- SIMILARITY: BELONGS TO THE SER/TAR FAMILY
CC CMK SUBFAMILY.
CC -----
CC -----

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EMBL: X63615; CAA45160.1; -.
PIR: A45025; A45025.
Uniprot: A45025.

DR HSE; Q63450; IAB5.
DR MGD; MGI:88257; Camk2b.
DR InterPro; IPR000719; Prot_kinase.

DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase

Q9db30 mus musculus
P22517 saccharomyc
Q06850 arabidopsis
P00518 oryctolagus
Q42844 schizosacch
Q16816 homo sapien
P31325 rattus norv
P12866 rattus norv
Q94547 schizosacch
P07934 mus musculus
Q38997 arabidopsis
P13349 homo sapien

[illegible][illegible]

- ! ENZYME REGULATION: AUTOPHOSPHORYLATION OF CMK-KINASE II PLAYS AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
- ! SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA, AND DELTA.
- ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CMK SUBFAMILY.

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CC	EMBL: X63613; CAA45160.1; .
DR	PIR: A45025; A45025.
DR	HSSP: C63450; 1A06.
DR	MGD: MGI:88257; Cank2b.
DR	InterPro: IPR000719; Prot_kinase.
DR	InterPro: IPR002290; Ser_thr_kinase.

DR PFam; PF000059; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO020; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; Serine/threonine-protein kinase; Calmodulin-binding;
KW

[illegible]

DE Xenopus laevis (African clawed frog); Vertebrata; Chordata; Vertebrata; Batrachia; Anura; Mesobatrachia; Pipiloidea; Sigidae; Xenocephalidae; Xenopus.
 NA [1]_Taxid:6355;
 NC SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Mandelstam E., Marilande H., Gavis J.;
 RT Differential expression of new calcium/calmodulin-dependent protein kinase II isoforms during Xenopus laevis oocyte maturation.*;
 RT Submitted FEB-2002 to the EMBL/Genbank/DBJ databases.
 CC EMBL: AF234631; Genbank: AF234631; DBJ: AF234631;
 CR EMBL: AF234631; Acc17556.1; -;
 DR HSP: G63450; I406; Prot.kinase.
 DR SWARTZ: A000001; Prot.kinase.
 DR InterPro: IPR000250; Sec. Thr. Kinase.
 DR Pfam: PF00669; pkinase.1.
 DR ProDom: P000001; Prot.kinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR KEGG: 091843; 62589 MW; 991843B36388317 CNE4;
 SQ SEQUENCE: 564 AA; 62589 MW; 991843B36388317 CNE4;

Query Match 83.8%, Score 2248.5, DB: 4, Length 564;
 Best Local Similarity 75.7%, Pred. No. 3e-173;
 Matches 441; Conservative 29; Mismatches 39; Indels 62; Gaps 7;
 QY 1 MATVTCFTFDTQYELGAGFASVRCVKYCTVHYAAKINTKLSARDKGLER 60
 DB 1 MATVTCFTFDTQYELGAGFASVRCVKYCTVHYAAKINTKLSARDKGLER 60
 QY 61 EATYCELLASNTVHDSISSEGFVFLVDTGSEFVARYETSEADASHCTQI 120
 DB 61 EATYCELLASNTVHDSISSEGFVFLVDTGSEFVARYETSEADASHCTQI 120
 QY 121 LEATVCHQVHVDLAFENLLKCKGNKAVLAFLAQVQDQAFATGPT 180
 DB 121 LEATVCHQVHVDLAFENLLKCKGNKAVLAFLAQVQDQAFATGPT 180
 QY 181 LSPFLKAKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 240
 DB 181 LSPFLKAKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 240
 QY 241 VTPKAKIYKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 300
 DB 241 VTPKAKIYKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 300
 QY 301 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 DB 301 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 QY 357 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 DB 357 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 QY 395 MLVQV - AGLLAKAGVQVFNSTAAATSTFQTFP - ALLESTFTVINYDPI 434
 DB 395 MLVQV - AGLLAKAGVQVFNSTAAATSTFQTFP - ALLESTFTVINYDPI 434
 QY 434 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 DB 434 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 QY 473 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 DB 473 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 QY 474 LVSDHKKFKFTENKLAHETKHTTLLNFTVYGERACNITREUTLNDGGRPT 513
 DB 474 LVSDHKKFKFTENKLAHETKHTTLLNFTVYGERACNITREUTLNDGGRPT 513
 QY 486 QSEETVWHREGRQVHFGSGAPAPQ 516
 DB 486 QSEETVWHREGRQVHFGSGAPAPQ 516
 QY 516 QSEETVWHREGRQVHFGSGAPAPQ 516
 DB 516 QSEETVWHREGRQVHFGSGAPAPQ 516

RESULT 8

Q88M13 PRELIMINARY; PRT; 527 AA.
 ID Q88M13
 DT 01-OCT-2002 (TRIMREL. 22, Created)
 DT 01-OCT-2002 (TRIMREL. 22, Last sequence update)
 DT 01-MAR-2003 (TRIMREL. 23, Last annotation update)
 CC 01-MAR-2003 (TRIMREL. 23, Last annotation update)
 NA [1]_Taxid:6355;
 NC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RT Submitted JUL-2002 to the EMBL/Genbank/DBJ databases.
 CC SWARTZ: A000001; Prot.kinase.
 CR EMBL: AF234631; Genbank: AF234631; DBJ: AF234631;
 DR HSP: G63450; I406; Prot.kinase.
 DR SWARTZ: A000001; Prot.kinase.
 DR InterPro: IPR000250; Sec. Thr. Kinase.
 DR Pfam: PF00669; pkinase.1.
 DR ProDom: P000001; Prot.kinase.1.
 DR SMART: S00220; S.F.K. 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR KEGG: 091843; 62589 MW; 991843B36388317 CNE4;
 SQ SEQUENCE: 527 AA; 62589 MW; 991843B36388317 CNE4;
 Query Match 82.8%, Score 2248.5, DB: 4, Length 527;
 Best Local Similarity 75.7%, Pred. No. 3e-173;
 Matches 439; Conservative 29; Mismatches 38; Indels 43; Gaps 4;
 QY 1 MATVTCFTFDTQYELGAGFASVRCVKYCTVHYAAKINTKLSARDKGLER 60
 DB 1 MATVTCFTFDTQYELGAGFASVRCVKYCTVHYAAKINTKLSARDKGLER 60
 QY 61 EATYCELLASNTVHDSISSEGFVFLVDTGSEFVARYETSEADASHCTQI 120
 DB 61 EATYCELLASNTVHDSISSEGFVFLVDTGSEFVARYETSEADASHCTQI 120
 QY 121 LEATVCHQVHVDLAFENLLKCKGNKAVLAFLAQVQDQAFATGPT 180
 DB 121 LEATVCHQVHVDLAFENLLKCKGNKAVLAFLAQVQDQAFATGPT 180
 QY 181 LSPFLKAKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 240
 DB 181 LSPFLKAKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 240
 QY 241 VTPKAKIYKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 300
 DB 241 VTPKAKIYKQVDFWAGVYLLVLTGPPFWDCHKYLQIAGATFFSPND 300
 QY 301 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 DB 301 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 QY 357 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 DB 357 KQALITLAFKFNFS - - - - - VGRQTATASATST 357
 QY 395 MLVQV - AGLLAKAGVQVFNSTAAATSTFQTFP - ALLESTFTVINYDPI 434
 DB 395 MLVQV - AGLLAKAGVQVFNSTAAATSTFQTFP - ALLESTFTVINYDPI 434
 QY 434 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 DB 434 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 QY 473 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 DB 473 KSTESQNTFEDENAKVQKILITELLINANNDEYATTCDCPELSPFELAN 473
 QY 474 LVSDHKKFKFTENKLAHETKHTTLLNFTVYGERACNITREUTLNDGGRPT 513
 DB 474 LVSDHKKFKFTENKLAHETKHTTLLNFTVYGERACNITREUTLNDGGRPT 513
 QY 486 QSEETVWHREGRQVHFGSGAPAPQ 516
 DB 486 QSEETVWHREGRQVHFGSGAPAPQ 516
 QY 516 QSEETVWHREGRQVHFGSGAPAPQ 516
 DB 516 QSEETVWHREGRQVHFGSGAPAPQ 516

SUMMARIES

Result	Score	# queries	Length	DB	ID	Description
1	222.5	82.0	565	4	US-08-100-960-2	Sequence 2, App
2	222.5	82.0	565	4	US-08-100-960-2	Sequence 2, App
3	1550	51.4	295	1	US-08-159-425-23	Sequence 23, Ap
4	1550	51.4	295	1	US-08-159-425-23	Sequence 23, Ap
5	1550	51.4	295	3	US-08-159-425-23	Sequence 23, Ap
6	1550	51.4	295	3	US-08-159-425-23	Sequence 23, Ap
7	1550	51.4	295	3	US-08-159-425-23	Sequence 23, Ap
8	1550	51.4	295	3	US-08-159-425-23	Sequence 23, Ap
9	1550	51.4	295	4	US-07-422-326-4	Sequence 23, Ap
10	1550	47.7	264	2	US-07-422-326-4	Sequence 23, Ap
11	619.5	22.6	355	4	US-08-159-664-10	Sequence 10, Ap
12	619.5	22.6	355	4	US-08-159-664-10	Sequence 10, Ap
13	619.5	22.6	355	4	US-08-159-664-10	Sequence 10, Ap
14	593	21.5	370	3	US-08-172-76-19	Sequence 19, Ap
15	593	21.5	370	3	US-08-172-76-19	Sequence 19, Ap
16	593	21.5	370	3	US-08-172-76-19	Sequence 19, Ap
17	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
18	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
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26	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
27	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
28	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
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30	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
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33	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
34	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
35	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
36	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
37	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
38	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
39	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
40	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
41	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
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45	558	20.6	463	1	US-07-404-31	Sequence 31, Ap
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ALIGNMENTS

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1  RESULT 1
2  US-08-900-960-2
3  Sequence 2, Application US/09800960
4  GENERAL INFORMATION:
5  1. APPLICANT: June et al
6  2. PARENT NO. 6387677
7  3. TITLE OF INVENTION: ACID MOLECULES
8  4. TITLE OF INVENTION: ACID MOLECULES
9  5. TITLE OF INVENTION: THEREOF
10 6. FILE REFERENCE: C1601158
11 7. CURRENT APPLICATION NUMBER: US/09/03-05
12 8. CURRENT FILING DATE: 2001-03-08
13 9. CURRENT FILING DATE: 2001-03-08
14 10. SOFTWARE: PARASQ for Windows Version 1.0
15 11. SEQ ID NO 2
16 12. LENGTH: 565
17 13. TYPE: PRT
18 14. ORGANISM: Human

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09 08. 8000 775 E. DO A. Tenath 565.

[illegible]

Best Local Similarity 52.48; Score 1450; DB 2; Length 295;
 Matches 27; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 14 YULVETGAGSVYRCKVCTGHTAAKINTKLSARHQRKREARICLLKHSNI 73
 Db 1 YULVETGAGSVYRCKVCTGHTAAKINTKLSARHQRKREARICLLKHSNI 60
 QY 74 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 133
 Db 61 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 120
 QY 61 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 120
 Db 134 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 193
 QY 134 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 193
 Db 121 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 180
 QY 194 PVDIMACGVITLLVFPFQDQKHQIQAGATGFFSPGVTTPKANKLNM 253
 Db 181 PVDIMACGVITLLVFPFQDQKHQIQAGATGFFSPGVTTPKANKLNM 240
 QY 254 TNPATGATBAKHPWCQSVASMSHQETVCEKFNARKKGLITM 308
 Db 241 TNPATGATBAKHPWCQSVASMSHQETVCEKFNARKKGLITM 295

RESULT 4
 US-08-459-448A-23
 Sequence 23; Application US/08459448A

GENERAL INFORMATION:
 APPLICANT: Kozel, Michael G.
 APPLICANT: Desai, Nalin M.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Crossland, Wade D.
 APPLICANT: Wright, Martin S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Rothwald, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Bader, Erik M.
 APPLICANT: Pace, Gary M.

INVENTOR: Kozel, Michael G.
 TITLE OF INVENTION: SYNTHETIC DNA SOURCE HAVING ENHANCED
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS: 520 White Plains
 STREET: Patent & Trademark Dept., 520 White Plains
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9605
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/459,448A
 FILING DATE: 07-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 07-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 NAME: Pace, Gary M.

REGISTRATION NUMBER: 44043
 REFERENCE/DOCKET NUMBER: C0C 1577/C11/CIIV4
 TELEPHONE: (919) 541-8582
 TELEFAX: (919) 541-8889
 INFORMATION: C0C 23:
 LENGTH: 295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear, single
 MOLECULE TYPE: protein
 HYPOTHEOICAL: NO
 NAME/KEY: Protein
 LOCATION: 1, 295
 OTHER INFORMATION: Protein sequence as shown in Figure 32.*
 US-08-459-448A-23

Query Match 53.48; Score 1450; DB 2; Length 295;
 Best Local Similarity 92.38; Pred. No. 9, seq-131; Indels 0; Gaps 0;
 Matches 27; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 14 YULVETGAGSVYRCKVCTGHTAAKINTKLSARHQRKREARICLLKHSNI 73
 Db 1 YULVETGAGSVYRCKVCTGHTAAKINTKLSARHQRKREARICLLKHSNI 60
 QY 74 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 133
 Db 61 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 120
 QY 61 VLHESISEGPHFLVDLVGSEFLVDVARETYSDAASHCIOQLVAVLKHGVY 120
 Db 134 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 193
 QY 134 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 193
 Db 121 HDLKEFLNLKSGAAKGLAVLQVQDQNGRFGSPOTSPYLKRVANGK 180
 QY 194 PVDIMACGVITLLVFPFQDQKHQIQAGATGFFSPGVTTPKANKLNM 253
 Db 181 PVDIMACGVITLLVFPFQDQKHQIQAGATGFFSPGVTTPKANKLNM 240
 QY 254 TNPATGATBAKHPWCQSVASMSHQETVCEKFNARKKGLITM 308
 Db 241 TNPATGATBAKHPWCQSVASMSHQETVCEKFNARKKGLITM 295

US-08-459-448A-23
 Sequence 23; Application US/08459448A

GENERAL INFORMATION:
 APPLICANT: Kozel, Michael G.
 APPLICANT: Desai, Nalin M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evans, Stephen V.
 APPLICANT: Crossland, Wade D.
 APPLICANT: Wright, Martin S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Bader, Erik M.
 APPLICANT: Pace, Gary M.

INVENTOR: Kozel, Michael G.
 TITLE OF INVENTION: SYNTHETIC DNA SOURCE HAVING ENHANCED
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS: 520 White Plains
 STREET: Patent & Trademark Dept., 520 White Plains
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9605
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/459,448A
 FILING DATE: 07-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 07-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 NAME: Pace, Gary M.

```

1 CITY: Fairytown
2 STATE: New York
3 COUNTRY: USA
4 PATENT NO: 607185
5 COMPETER READABLE FORM:
6
7 MEDIUM TYPE: Floppy disk
8 MEDIUM TYPE: PC DOS/MS DOS
9 OPERATING SYSTEM: PC DOS/MS DOS
10 SOFTWARE: PatentIn Release #1.0, Version #1.30
11 CURRENT APPLICATION DATA: US 08/459,595A
12 FILING DATE: 02-JUN-1995
13 CLASSIFICATION: 800
14 APPLICATION NUMBER: US 07/951,715
15 PRIORITY DATE: 25-SEP-1992
16 APPLICATION NUMBER: US 07/772,027
17 FILING DATE: 04-OCT-1991
18 AUTOMATED INFORMATION:
19 REFERENCE/DOCKET NUMBER: 40403
20 REFERENCE/DOCKET NUMBER: CSC 1577/CIP/DIV3
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (519)541-8689
23 INFORMATION FOR SEQ ID NO: 23:
24 SOURCE: Chem. Abstr.
25 LENGTH: 295 amino acids
26 TYPE: amino acid
27 STRANDNESS: single
28 MOLECULE TYPE: protein
29 HYPOTHETICAL: NO
30 NAME/KEY: Protein
31 LOCATION: 1..295
32 OTHER INFORMATION: /note="rat protein kinase II"
33 OTHER INFORMATION: Protein sequence as shown in Figure 32.*
34
35 US-08-459-595a-23
36
37 Query Match 53.48; Score 1450; DB 3; Length 295;
38 Best Local Similarity 52.54; Pred. No. 9.6e-131;
39 Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
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41 QY 14 YQVLEEDGAGSVVRVCVLCVTCVETAAKINTKLSRHQVLEAEATCRKLKSHNI 73
42 DB 1 YQVLEEDGAGSVVRVCVLCVTCVETAAKINTKLSRHQVLEAEATCRKLKSHNI 60
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44 QY 74 VLEDSISESGHYFLVPLVTCVGELEFVIVARYETSEADSHCQDIIHLAVLCHQNYV 133
45 DB 1 VLEDSISESGHYFLVPLVTCVGELEFVIVARYETSEADSHCQDIIHLAVLCHQNYV 120
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47 QY 61 VLEDSISESGHYFLVPLVTCVGELEFVIVARYETSEADSHCQDIIHLAVLCHQNYV 120
48 DB 134 HDLAPNGLKLSKAQKLAQGLAFCVGLQVQGMQAFAGFPGLSPVLEKAYGK 193
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50 QY 121 HDLAPNGLKLSKAQKLAQGLAFCVGLQVQGMQAFAGFPGLSPVLEKAYGK 180
51 DB 121 HDLAPNGLKLSKAQKLAQGLAFCVGLQVQGMQAFAGFPGLSPVLEKAYGK 180
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53 QY 134 PDQTRAGVLTLLVTPFDQDQKLYQIAGATFFSSQDQVTPFAKLIHQML 253
54 DB 134 PDQTRAGVLTLLVTPFDQDQKLYQIAGATFFSSQDQVTPFAKLIHQML 240
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56 QY 181 FPDNAGVLLVLTQVTPFDQDQKLYQIAGATFFSSQDQVTPFAKLIHQML 240
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59 QY 234 TNPAPATDQQLHAWQVQSVASNMHROVTECLAKFPAKRLKALITN 308
60 DB 234 TNPAPATDQQLHAWQVQSVASNMHROVTECLAKFPAKRLKALITN 308
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REFERENCE/DOCKET NUMBER: S-18005H
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 01515-41-1587
 FAX: 01515-41-1589
 INFORMATION FOR SEQ ID NO: 23
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241
 TYPE: amino acid
 STRANDNESS: single
 WILDFOLD: linear
 HYPOTHEICAL: NO
 FEATURE:
 CDS/GENE: Protein
 LOCATION: 1..295
 OTHER INFORMATION: /note="rat protein kinase II
 protein sequence as shown in Figure 32."
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 51.48; Score 1450; DB 4; Length 295;
 Identical Similarity 52.5%; Pred No. 9,6e+13; Mismatches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 14 VQLVDEKGFQSVVPRVVCVLCQGVKATIKFLKSNDRQKLEKARICELLKEPPI 73
 Db 1 VQLFDEKGFQSVVPRVVCVLCQGVKATIKFLKSNDRQKLEKARICELLKEPPI 73
 QY 74 VLRHSISSESGFVPLVPLGCELPDI VAREYVSADASNCIQQLLEAVRHQWY 133
 Db 61 VLRHSISSESGFVPLVPLGCELPDI VAREYVSADASNCIQQLLEAVRHQWY 120
 QY 134 HDLPFELLKASKGAVALDFGLAEVQSDQANQFSGTGLSPVLEKEAY 193
 Db 121 HDLPFELLKASKGAVALDFGLAEVQSDQANQFSGTGLSPVLEKEAY 180
 QY 194 PVDIMAGCVLTLLVGPFPFDEQDKIQTKAGATDFFPMDVTPPEAKNLNQ 253
 Db 181 PVDIMAGCVLTLLVGPFPFDEQDKIQTKAGATDFFPMDVTPPEAKNLNQ 240
 QY 254 TTPARKITDQALHFWQVQSTVAMRGRKFTVELLKPFARKIKGALITM 308
 Db 241 TTPARKITDQALHFWQVQSTVAMRGRKFTVELLKPFARKIKGALITM 295

RESULT 9
 US-07-857-2248-19
 : Sequence 19, Application US/07857224B
 : Patent Classifications: 114
 : GENERAL INFORMATION:
 : APPLICANT: Benner, Steven A.
 : NUMBER OF SEQUENCES: 114
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Steven A. Benner
 : COUNTRY: Switzerland
 : CITY: Zurich
 : STATE: none
 : ZIP CODE: This is an international post code CH-8092
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
 : OPERATING SYSTEM: Macintosh 7.0
 : SOFTWARE: Microsoft Word
 : CURRENT APPLICATION DATA:
 : FILING DATE: 03/25/92
 : CLASSIFICATION: 436
 : PUBLICATION INFORMATION:
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (international) 41 1 632 2830
 : TELEFAX: (international) 41 1 262 2437

TELEX: none
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241
 TYPE: amino acid
 STRANDNESS: linear
 WILDFOLD: linear
 HYPOTHEICAL: NO
 FEATURE:
 CDS/GENE: protein
 LOCATION: rat
 OTHER INFORMATION: /note="rat protein kinase; Table 8 Column 21
 protein sequence as shown in Figure 32."
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 12 DEQVLDKGFQSVVPRVVCVLCQGVKATIKFLKSNDRQKLEKARICELLKEPPI 71
 Db 1 DEQVLDKGFQSVVPRVVCVLCQGVKATIKFLKSNDRQKLEKARICELLKEPPI 60
 QY 72 NVLRHSISSESGFVPLVPLGCELPDI VAREYVSADASNCIQQLLEAVRHQWY 131
 Db 61 NVLRHSISSESGFVPLVPLGCELPDI VAREYVSADASNCIQQLLEAVRHQWY 120
 QY 132 VYRDLFELLKASKGAVALDFGLAEVQSDQANQFSGTGLSPVLEKEAY 191
 Db 121 VYRDLFELLKASKGAVALDFGLAEVQSDQANQFSGTGLSPVLEKEAY 180
 QY 192 GPVDDIMAGCVLTLLVGPFPFDEQDKIQTKAGATDFFPMDVTPPEAKNLNQ 251
 Db 181 GPVDDIMAGCVLTLLVGPFPFDEQDKIQTKAGATDFFPMDVTPPEAKNLNQ 240
 QY 252 MCTINPARKITDQALHFWQVQSTVAMRGRKFTVELLKPFARKIKGALITM 275
 Db 241 MCTINPARKITDQALHFWQVQSTVAMRGRKFTVELLKPFARKIKGALITM 264

RESULT 10
 US-07-857-2248-18
 : Sequence 18, Application US/07857224B
 : Patent Classifications: 114
 : GENERAL INFORMATION:
 : APPLICANT: Benner, Steven A.
 : TITLE OF INVENTION: Predicting Folded Structures of Proteins
 : NUMBER OF SEQUENCES: 114
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Steven A. Benner
 : COUNTRY: Switzerland
 : CITY: Zurich
 : STATE: none
 : ZIP CODE: This is an international post code CH-8092
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
 : OPERATING SYSTEM: Macintosh 7.0
 : SOFTWARE: Microsoft Word
 : CURRENT APPLICATION DATA:
 : FILING DATE: 03/25/92
 : CLASSIFICATION: 436
 : PUBLICATION INFORMATION:
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (international) 41 1 632 2830
 : TELEFAX: (international) 41 1 262 2437

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/ TELCOMMUNICATION INFORMATION:
/   TELEPHONE (International): 1 1 632 2890
/   TELEPHONE (Domestic): 1 1 632 2890
/   FAX (International): 1 1 632 2897
/   FAX (Domestic): 1 1 632 2897
/   INFORMATION FOR SEQ ID NO: 18:
/     SOURCE: GenBank
/     LENGTH: 261
/     TYPE: amino acid
/     TOPOLOGY: linear
/     DESCRIPTION: protein
/     ORIGINAL SOURCE:
/       ORGANISM: Homo sapiens
/       TISSUE: muscle
/       STRAIN: C2C12
/       CELL: C2C12
/       PASSAGE: 1
/     PUBLICATION INFORMATION:
/       PUBLISHED IN: Journal of Cell Biology
/       AUTHOR: Hanke, S. K.
/       AUTHOR: Quirin, A. K.
/       AUTHOR: Hunter, T.
/       TITLE: The protein kinase family
/       JOURNAL: J. Biol. Chem.
/       VOLUME: 241
/       PAGES: 42-52
/       YEAR: 1996
/     QUERY MATCH: 47.74; Score 124.1; DB 2; Length 264;
/     BERT LOCAL SIMILARITY: 39.54; Pred. No. 5,6e-51;
/     MISMATCHES: 15; Conservative: 15; Mismatches: 10; Indels: 0; Gaps: 0;
/
/ QY 12 EHQVWIDYQKASGVYKCVKCHETAKIKTKLKHGKQWSEKFKLHMS 71
/ Db 1 EHQVWIDYQKASGVYKCVKCHETAKIKTKLKHGKQWSEKFKLHMS 71
/
/ QY 72 NYVLEHSTSEGHVITWQVTCSELEFDIVARVTSKASHCQGLIAYLKHGMS 131
/ Db 61 NYVLEHSTSEGHVITWQVTCSELEFDIVARVTSKASHCQGLIAYLKHGMS 120
/
/ QY 133 VYHEDLFPNLLASKGKANKLADGCLAGIAYLKHGMSQWSEKFKLHMS 191
/ Db 121 VYHEDLFPNLLASKGKANKLADGCLAGIAYLKHGMSQWSEKFKLHMS 180
/
/ QY 192 GNPDVTCVYKTLVCTPPQDQHQHLYKQAGATVDFSPQVTFEAKMLND 251
/ Db 181 GNPDVTCVYKTLVCTPPQDQHQHLYKQAGATVDFSPQVTFEAKMLND 240
/
/ QY 252 MTPINAKTIVHAKLGHFWKQV 275
/ Db 241 MTPINAKTIVHAKLGHFWKQV 264
/
/ RESULT 11
/   QUERY MATCH: 47.74; Score 124.1; DB 2; Length 264;
/   BERT LOCAL SIMILARITY: 39.54; Pred. No. 5,6e-51;
/   MISMATCHES: 15; Conservative: 15; Mismatches: 10; Indels: 0; Gaps: 0;
/   SEQUENCE 10: Application US/09579664B
/   GENERAL INFORMATION:
/     APPLICANT: Genentech, Inc.
/     APPLICANT: Birm, Jennifer L.
/     APPLICANT: Corley, Neil C.
/     APPLICANT: Gugler, Karl C.
/     APPLICANT: Goli, Surya K.
/     APPLICANT: Shah, Puri
/     TITLE OF INVENTION: KINASE ASSOCIATED PROTEIN
/     TITLE OF INVENTION: KINASE
/     NUMBER OF SEQUENCES: 21
/     CORRESPONDENCE ADDRESS:
/       GENENTECH, INC.
/       STREET: 3174 Porter Drive
/       CITY: Palo Alto
/       STATE: CA
/       ZIP: 94304
/     COMPUTER READABLE FORM:
/       FILE NAME: 09579664B
/       COUNTER: 100
/       OPERATING SYSTEM: DOS
/       SOFTWARE: FASTA for Windows Version 2.0
/       APPLICATION NUMBER: US/08/075,969
/     FILING DATE: 04/07/98
/     CLASSIFICATION: 435
/     APPLICATION NUMBER:
/     FILING DATE:
/     FILING DATE:
/     NAME: ALLIANT
/     REGISTRATION NUMBER: 36,749
/     REFERENCE/DOCKET NUMBER: PP-0321 US
/     REFERENCE/DOCKET NUMBER:
/     TELEPHONE: 415-855-0955
/     TELEFAX: 415-845-4166
/     TELETYPE:
/     FPO SEQ ID NO: 19;
/     SEQUENCE CHARACTERISTICS:

```

LENGTH: 370 amino acids
 STRANDNESS: alpha/beta
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 ORGANISM: Human
 CLONE: 790790
 US-08-978-989-19

Query Match
 Best Local Similarity 21.5%; Score 583; DB 2; Length 370;
 Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;
 QY 12 DFLVQVLDGKAGVSV-----RCVLCGCHETAKINKLKSARHQLREARICR 66
 DB 18 DITDFPFLVGTGAGSESVILAKDKFQKLV-----VAICIAKALAKE-GSMEINIAVL 71
 QY 67 LKSENIVLHNSISSEGRH-VLPDVLVYGLFELPDAVNTSADSHCQIQLNVL 125
 DB 72 KHEINIVL-VDTTSGHMLDQVSGSLPFLVYKGTFTGASRLFOYLAK 130
 QY 136 HKQGVNVAAGKAVKASKGKAVKAPGLAFLVQVQDQAGTACTGCTLSPEV 185
 DB 131 YLHGLVYHKLKFNLLYSLDKSKHISNGLS-KMEQPSVYCTACTGCTVAYEV 189
 QY 186 LREAAGVQVIRAGVYLVVYPPFDQKLVQIACAGTDFSPRQVTPPEA 245
 DB 190 LAQVPSKAVQSGVYVILVGLQPTTIDENDALFQVLIKAEYTFPSPTWDDISDA 249
 QY 246 KNLNQMTINARLTAEBAKHPVQSRVSAVMHQRQVETCLAKFNKRLKGL 305
 DB 250 KQVFLHAKQEPRTCDQALQHPFADCTALNKH-KQSVRSKKNFASKKQAFN 308
 QY 306 TT-----MLATRFVSQVITPAIATAASCTMG 336
 DB 309 ANVYVRMKLQGTSCQGTASHELITVWAGSPAG 348

RESULT 13
 Sequence 19, Application US/0327296

GENERAL INFORMATION:
 APPLICANT: Bundesas, Olga
 APPLICANT: Cortinas, Maricfer L.
 APPLICANT: Guejlar, Karl G.
 APPLICANT: Lal, Presti
 APPLICANT: Shah, Puri K.
 APPLICANT: Singh, Puri
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 ADDRESSEE: Inocyte Pharmaceuticals, Inc.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 COMPILED BY: 643104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSBO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: 05/09/2002
 FILING DATE: 05/09/2002
 CLASSIFICATION:
 PUBLICATION DATA:
 APPLICATION NUMBER: 09/878,989
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J J
 OFFICE ADDRESS: MEMPHIS, TN 38176
 TELEPHONE: 901-527-7746
 TELECOMMUNICATION INFORMATION: PP-0321 US
 TELEPHONE: 415-852-0555
 TELEFAX: 415-845-4106
 TEXT:
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 ORGANISM: Human
 CLONE: 790790
 US-09-272-796-19

Query Match
 Best Local Similarity 35.1%; Pred. No. 1.9e-47;
 Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;
 QY 12 DFLVQVLDGKAGVSV-----RCVLCGCHETAKINKLKSARHQLREARICR 66
 DB 18 DITDFPFLVGTGAGSESVILAKDKFQKLV-----VAICIAKALAKE-GSMEINIAVL 71
 QY 67 LKSENIVLHNSISSEGRH-VLPDVLVYGLFELPDAVNTSADSHCQIQLNVL 125
 DB 72 KHEINIVL-VDTTSGHMLDQVSGSLPFLVYKGTFTGASRLFOYLAK 130
 QY 136 HKQGVNVAAGKAVKASKGKAVKAPGLAFLVQVQDQAGTACTGCTLSPEV 185
 DB 131 YLHGLVYHKLKFNLLYSLDKSKHISNGLS-KMEQPSVYCTACTGCTVAYEV 189
 QY 186 LREAAGVQVIRAGVYLVVYPPFDQKLVQIACAGTDFSPRQVTPPEA 245
 DB 190 LAQVPSKAVQSGVYVILVGLQPTTIDENDALFQVLIKAEYTFPSPTWDDISDA 249
 QY 246 KNLNQMTINARLTAEBAKHPVQSRVSAVMHQRQVETCLAKFNKRLKGL 305
 DB 250 KQVFLHAKQEPRTCDQALQHPFADCTALNKH-KQSVRSKKNFASKKQAFN 308
 QY 306 TT-----MLATRFVSQVITPAIATAASCTMG 336
 DB 309 ANVYVRMKLQGTSCQGTASHELITVWAGSPAG 348

RESULT 14
 Sequence 14, Application US/04570408

GENERAL INFORMATION:
 APPLICANT: Inocyte Pharmaceuticals Incorporated
 APPLICANT: Heilon, Steve
 TITLE OF INVENTION: Crystallized P38 Complexes
 TITLE OF INVENTION: Crystallized P38 Complexes
 CURRENT APPLICATION NUMBER: US/09/457,0408
 CURRENT FILING DATE: 1999-12-08
 NUMBER OF SEQ ID NOS: 41
 SEQUENCE INFORMATION:
 SEQ ID NO 31
 LENGTH: 370
 ORGANISM: Human
 US-09-457-0408-31

Query Match
 Best Local Similarity 35.1%; Pred. No. 1.9e-47;
 Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;
 QY 12 DFLVQVLDGKAGVSV-----RCVLCGCHETAKINKLKSARHQLREARICR 66
 DB 18 DITDFPFLVGTGAGSESVILAKDKFQKLV-----VAICIAKALAKE-GSMEINIAVL 71


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QY 67 LKHNHVLHDSISEDFH-LVFDVLVGGELFVARETTERADACSHQIILNVL 125
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Db 72 KLEHFNAL-VGLTESGGLLQVQSGGLLQVQSGGLLQVQSGGLLQVQSGGL 130
QY 136 RCHQGVVHEDKQFNILLAKCKKQKAVKLAQGLAEVQGGQAGAPGLISPV 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 LKEDGTVHDLVFNLYLSIDSSKLSINSSKLS-KNEVGSVLSTNGKGVADV 189
QY 186 LKKEATQVQKAGQVLLVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 LAKFETKQVDSGVVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 249
QY 246 KVLKQVHETKQVDSGVVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 KQFVHLEHEDKPKFTCEALQVFPAGDIALKNGH-QSVSLKKNFASKKQAFN 308
QY 306 FT-----WAKRNSVCHQVFAKNSAKSTQVQ 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 ATATVHBMALQVTSRQGGQVASHGELLFVAGGPAAG 348

RESULT 15
US-09-575-326-4
: Patent No. 6476210
: GENERAL INFORMATION:
: APPLICANT: Pfizer, Inc.
: INVENTOR: Alexander Jr.
: TITLE OF INVENTION: No. 6476210a1 Human Kinases and Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0234-US
: CURRENT FILING DATE: 2004-10-11
: PRIOR APPLICATION NUMBER: US 60/239,621
: PRIORITY DATE: 2000-10-12
: KNOWN FILERS DATE: 2000-10-12
: SOFTWARE: FastS80 for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 465
: TYPE: PRT
: ORGANISM: homo sapiens
: US-09-575-326-4

Query Match 21.4%; Score 582; DB 4; Length 765;
Best Local Similarity 34.6%; Fred. No. 7.4e-47;
Matches 131; Conservative 70; Mismatches 154; Indels 24; Gaps 6;
QY 12 DEVDLDELGGAVSVBQVLCVGTGHTPAKILNFKLSADQKQKLEPKRILKHS 71
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 351 ENKAGVLDQVNVVHEDSGVDSGLLQVQSGGLLQVQSGGLLQVQSGGL 449
QY 72 NIVRHDSISEDFH-LVFDVLVGGELFVARETTERADACSHQIILNVL 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 450 NIKLVENETATELVHEDSGVDSGLLQVQSGGLLQVQSGGLLQVQSGGL 509
QY 132 VVHDLDELGGAVSVBQVLCVGTGHTPAKILNFKLSADQKQKLEPKRILKHS 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 510 IVYDQVDELGGAVSVBQVLCVGTGHTPAKILNFKLSADQKQKLEPKRILKHS 566
QY 131 YKQVQVNDQVLYVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 567 YKLAQVNDQVLYVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 626
QY 249 TQKQVTPKATVHARL-KHFNQVSVASVMSHGVVELKFNKRAKGLITPM 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 627 ISQVQVNTKACTAGQVLPVSDQSGVQVQVQVQVQVQVQVQVQVQVQV 666
QY 309 LATVHETKQVDSGVVILVQVPPVNDQKRLQIQAGANQVSPSPVTPER 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 SYVNTALKE-----QVTSKQKQSGH-QMPE-ISPVPVSELVFV 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 KQVLPALQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 387
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Db = 730 PGENVAPTPSPSPHPT 748

Search completed: October 10, 2003, 08:12:05
Job time : 27 sec

GenCode version 5.1.6
Copyright (c) 1995-2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2003, 08:08:11 ; Search time 350 Seconds
(without alignments)
352.469 Million cell updates/sec

Title: US-09-820-790-2
Sequences: 2 MATVCTCFDEPQVLYEDT.....DOWNKVFHFCASVAPDQ 516

Scoring table: BLASTNM2
Gapop 10.0 , Gapext 0.5

Searched: 600633 seeds, 161128416 residues

Total number of hits satisfying chosen parameters: 600633

Minimum DB seq length: 0
Maximum DB seq length: 400000000

Post-processing: Minimum match 0%
Maximum match 100%
Listing first 43 summaries

Database : Published_Applications_Aa**

- 1: /cgn2.6/prodata/2/pub/paa/US07_PUBCOMB.pep.*
- 2: /cgn2.6/prodata/2/pub/paa/US06_NEW_PUB.pep.*
- 3: /cgn2.6/prodata/2/pub/paa/US06_NEW_PUB.pep.*
- 4: /cgn2.6/prodata/2/pub/paa/US06_PUBCOMB.pep.*
- 5: /cgn2.6/prodata/2/pub/paa/US06_PUBCOMB.pep.*
- 6: /cgn2.6/prodata/2/pub/paa/US06_PUBCOMB.pep.*
- 7: /cgn2.6/prodata/2/pub/paa/US08_NEW_PUB.pep.*
- 8: /cgn2.6/prodata/2/pub/paa/US08_PUBCOMB.pep.*
- 9: /cgn2.6/prodata/2/pub/paa/US08_PUBCOMB.pep.*
- 10: /cgn2.6/prodata/2/pub/paa/US09_PUBCOMB.pep.*
- 11: /cgn2.6/prodata/2/pub/paa/US09_PUBCOMB.pep.*
- 12: /cgn2.6/prodata/2/pub/paa/US10_NEW_PUB.pep.*
- 13: /cgn2.6/prodata/2/pub/paa/US10_PUBCOMB.pep.*
- 14: /cgn2.6/prodata/2/pub/paa/US10_PUBCOMB.pep.*
- 15: /cgn2.6/prodata/2/pub/paa/US10_PUBCOMB.pep.*
- 16: /cgn2.6/prodata/2/pub/paa/US10_PUBCOMB.pep.*
- 17: /cgn2.6/prodata/2/pub/paa/US10_NEW_PUB.pep.*
- 18: /cgn2.6/prodata/2/pub/paa/US10_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	ID	Description
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2	2675	99.2	516	12	US-09-820-790-2
3	2325	88.2	516	12	US-09-820-790-2
4	2205	81.2	556	14	US-10-056-950-4
5	2070	76.2	499	12	US-10-354-358-88
6	1875	68.2	499	12	US-10-354-358-88
7	1174	43.1	261	9	US-09-925-928-83
8	1174	43.1	261	11	US-09-925-299-983
9	619.5	22.8	355	12	US-10-352-975-10
10	619.5	22.8	355	12	US-10-352-975-10
11	613.5	22.6	357	15	US-10-024-0365-2
12	384.5	21.5	467	11	US-09-935-484-3
13	384.5	21.5	467	11	US-09-935-484-3
14	384.5	21.5	467	11	US-10-125-835-3
15	384.5	21.5	476	15	US-10-125-835-5

16	583	21.5	370	10	US-09-817-181-4
17	583	21.5	370	12	US-09-769-970-19
18	583	21.5	370	12	US-09-769-970-19
19	583	21.5	370	12	US-10-024-041-10
20	583	21.5	370	15	US-10-142-356-7
21	583	21.5	370	15	US-10-142-356-7
22	583	21.5	370	15	US-10-300-826-4
23	583	21.5	370	15	US-10-300-826-4
24	582	21.4	766	10	US-09-915-326-2
25	582	21.4	766	10	US-09-915-326-2
26	582	21.4	766	12	US-10-171-085-2
27	582	21.4	766	15	US-10-171-085-2
28	577.5	21.3	317	11	US-09-925-466-36
29	577.5	21.3	317	11	US-09-925-466-36
30	566.5	20.9	495	12	US-10-299-375-16
31	566.5	20.9	495	12	US-09-848-806-1
32	561.5	20.7	501	12	US-10-289-372-3
33	561.5	20.7	501	12	US-10-289-372-3
34	558	20.6	463	10	US-09-988-463-25
35	548	20.2	406	10	US-09-771-16A-210
36	548	20.2	406	10	US-09-771-16A-210
37	546.5	20.1	326	10	US-09-817-181-2
38	546.5	20.1	326	12	US-10-090-002-2
39	546.5	20.1	326	15	US-10-300-826-3
40	546.5	20.1	326	15	US-10-300-826-3
41	545	20.1	501	9	US-09-797-039-2
42	543	20.1	501	12	US-10-170-785-2
43	543	20.1	501	12	US-10-170-785-2
44	541	19.9	648	15	US-09-688-537-38
45	541	19.9	648	15	US-10-024-0368-5

ALIGNMENTS

RESULT 1
US-09-820-790-2
; Sequence 2, Application US/09820790
; Sequence 2, Application US/09820790
; GENERAL INFORMATION: US/09820790
; TITLE: INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACIDS, AND COMPOSITIONS THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01204
; CURRENT PUBLICATION NUMBER: US/09/820,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatSeq for Windows Version 1.0
; SEQNO: 516
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Human
US-09-820-790-2

Query Match
Residue Similarity 100.0%, Pred. MO. 1,3e-217;
Residue 516, Conservative 0, Alignments 0, Indels 0; Gaps 0;

0y	1	MATVCTCFDEPQVLYEDTAKGAFVYRVCVLCGKGTAKIMTKGADKDKLER	60
Db	1	MATVCTCFDEPQVLYEDTAKGAFVYRVCVLCGKGTAKIMTKGADKDKLER	60
0y	61	EARICCKHNTVLMQDSISEDFIVDFGDEFDIATBTSEADASHCQQI	120
Db	61	EARICCKHNTVLMQDSISEDFIVDFGDEFDIATBTSEADASHCQQI	120
0y	121	LEAVLKHOMVHEKLLKACIKGKAGVLAFLGADGQDNFAGSTGR	180
Db	121	LEAVLKHOMVHEKLLKACIKGKAGVLAFLGADGQDNFAGSTGR	180
0y	181	LSPPVAKKAGKGVLMACGVITLVGVFWPMDQKIQDQKAGATPSPDPT	240
Db	181	LSPPVAKKAGKGVLMACGVITLVGVFWPMDQKIQDQKAGATPSPDPT	240

QY 435 -----FTENLANSKSTHTLTHVHVGEDACIATRLQY 475
 Db 465 TFEPEALGVLEMDPHKFTFENLANSKSKSTHTLTHVHVGEDACIATRLQY 524
 QY 476 IDGQGFRTGQSEFTVWHRQGNWHLNWHSCAPALQ 516
 Db 525 IDGQGFRTGQSEFTVWHRQGNWHLNWHSCAPALQ 565

RESULTS 4
 US-10-094-960-4
 : Sequence 4, Application US/10094960
 : Publication No. US20020132241
 : APPLICANT: Yeh, Jane et al.
 : TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
 : THEREOF
 : FILE REFERENCE: C0001188DV
 : CURRENT APPLICATION NUMBER: US/10-096 960
 : PRIOR APPLICATION NUMBER: 09/800 960
 : PRIOR FILING DATE: 2001-03-08
 : NUMBER OF SEQ ID NOS: 4
 : SEQ ID NO 4: RASLSDQ for Windows Version 4.0
 : LENGTH: 596
 : ORGANISM: Homo sapien
 US-10-094-960-4

Query Match 81.24; Score 2205; DB 31; Length 596;
 Best Local Similarity 74.24; Pred. No. 4.3e-175;
 Matches 431; Conservative 25; Mismatches 35; Indels 90; Gaps 5;
 Db 1 MATTTCTCTFTVQLDVGKQSVYKVTSTQAKTIKTLASQKHLER 60
 QY 1 MATTTCTCTFTVQLDVGKQSVYKVTSTQAKTIKTLASQKHLER 60
 Db 61 EATCKLHSHVYLDUSISSEGFVFLVDTVGLGEFVAVETSEADNSCIQI 120
 QY 61 EATCKLHSHVYLDUSISSEGFVFLVDTVGLGEFVAVETSEADNSCIQI 120
 Db 121 LEATLCHQGVHVDLKEFLNLSKCKGKAVLAFLAIVQDQGNQFAGTGY 180
 QY 121 LEATLCHQGVHVDLKEFLNLSKCKGKAVLAFLAIVQDQGNQFAGTGY 180
 Db 122 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 180
 QY 181 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 240
 Db 181 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 240
 QY 241 VPEKALNQLMTNARTEALHAPKFWQGVSTVSMHSEFTVCLAKFNARKL 300
 Db 241 VPEKALNQLMTNARTEALHAPKFWQGVSTVSMHSEFTVCLAKFNARKL 300
 QY 301 KQALITLMTLAFNFSVQRTAPATSTASITMSLVQAKSLAKED- QNFQFST 359
 Db 301 KQALITLMTLAFNFSVQRTAPATSTASITMSLVQAKSLAKED- QNFQFST 359
 QY 360 KKNKAAVSGKTFEPALAGKQVTVMPQGTKESSQSNATFTEDAKA 409
 Db 336 KNSVLAQAGAPQGTMTQPTVWHAQDITKSTSTSTEDTDLDAFLPTGSS 359
 QY 410 -----RQKQVLTALANLVNQHGVAV 434
 Db 396 VPEKASDQRTASQMGQVFCSSAMPKQKSTFTLEALNKKQFATYICDGL 455
 QY 435 -----FTENLANSKSTHTLTHVHVGEDACIATRLQY 475
 Db 456 TFEPEALGVLEMDPHKFTFENLANSKSTHTLTHVHVGEDACIATRLQY 524
 QY 476 IDGQGFRTGQSEFTVWHRQGNWHLNWHSCAPALQ 516

Db 516 IDGQGFRTGQSEFTVWHRQGNWHLNWHSCAPALQ 556

RESULTS 5
 US-10-354-358-88
 : Sequence 88, Application US/10354358
 : Publication No. US2002039357062A1
 : GENERAL INFORMATION:
 : APPLICANT: Millenium Pharmaceuticals, Inc
 : APPLICANT: Hunter, John Joseph
 : APPLICANT: Hunter, John Joseph
 : APPLICANT: Tsai, Feng-Ying
 : APPLICANT: Leskow, Andrea
 : APPLICANT: Leskow, Andrea
 : APPLICANT: Kallio, Marko
 : APPLICANT: Rudolph/Women, Laura A.
 : TITLE OF INVENTION: METRINS AND COMPOSITIONS FOR TREATING
 : METRINIC ACID DEFICIENCY
 : TIME OF INVENTION: 7181, 7650, 25641, 65583, 49863, 8857, 1682, 1767, 9235,
 : TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2089, 32427, 2160,
 : TITLE OF INVENTION: 8959, 3189, 9288, 8528, 9288, 9288, 9288, 3320, 1156, 4943,
 : TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 3420, 32316, 2059,
 : TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66438 MOLECU
 : CURRENT APPLICATION NUMBER: US/10/354 358
 : CURRENT FILING DATE: 2003-01-30
 : PRIOR APPLICATION NUMBER: US 60/353,600
 : PRIOR FILING DATE: 2002-01-31
 : PRIOR APPLICATION NUMBER: US 60/264,517
 : PRIOR FILING DATE: 2002-03-15
 : PRIOR APPLICATION NUMBER: US 60/371,075
 : PRIOR FILING DATE: 2002-04-09
 : PRIOR APPLICATION NUMBER: US 60/371,507
 : PRIOR FILING DATE: 2002-04-16
 : PRIOR APPLICATION NUMBER: US 60/372,984
 : PRIOR FILING DATE: 2002-04-16
 : PRIOR APPLICATION NUMBER: US 60/374,194
 : PRIOR FILING DATE: 2002-05-24
 : PRIOR APPLICATION NUMBER: US 60/385,033
 : PRIOR FILING DATE: 2002-05-24
 : PRIOR APPLICATION NUMBER: US 60/386,853
 : PRIOR FILING DATE: 2002-06-14
 : PRIOR APPLICATION NUMBER: US 60/389,395
 : PRIOR FILING DATE: 2002-06-37
 : Remaining Prior Application data removed - See File Wrapper or PALM.
 : NUMBER OF SEQ ID NOS: 122
 : SEQ ID NO 88
 : ORGANISM: Homo sapiens
 US-10-354-358-88

Query Match 74.24; Score 2070; DB 12; Length 499;
 Best Local Similarity 73.13; Pred. No. 6.4e-164;
 Matches 396; Conservative 31; Mismatches 25; Indels 90; Gaps 3;
 Db 1 MATTTCTCTFTVQLDVGKQSVYKVTSTQAKTIKTLASQKHLER 60
 QY 1 MATTTCTCTFTVQLDVGKQSVYKVTSTQAKTIKTLASQKHLER 60
 Db 61 EATCKLHSHVYLDUSISSEGFVFLVDTVGLGEFVAVETSEADNSCIQI 120
 QY 61 EATCKLHSHVYLDUSISSEGFVFLVDTVGLGEFVAVETSEADNSCIQI 120
 Db 61 EATCKLHSHVYLDUSISSEGFVFLVDTVGLGEFVAVETSEADNSCIQI 120
 QY 121 LEATLCHQGVHVDLKEFLNLSKCKGKAVLAFLAIVQDQGNQFAGTGY 180
 Db 121 LEATLCHQGVHVDLKEFLNLSKCKGKAVLAFLAIVQDQGNQFAGTGY 180
 QY 122 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 180
 Db 122 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 180
 QY 181 LSVNVLKMDVYHGLAFYLLASLAKGKAVLAFLAIVQDQGNQFAGTGY 240


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; NAME/SEQ: SITE
; LOCATION: (259)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (260)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-239-953

Query Match
Best Local Similarity 43.28; Score 1174; DB 9; Length 261;
Matches 230; Conservative 11; Mismatches 8; Indels 64; Gaps 2;
QY 5 VGGSELEPTVARYTSADASHCTQITLAVLICHQGVVDEHGLPNNLLASKKAA 152
Db 1 VTGGSELEPTVARETSADASHCTQITLAVLICHQGVVDEHGLPNNLLASKKAA 60
QY 135 VLADGALAEVQDQDQAFQVPSVLRKAGQVPMWACVQVITLLVGP 212
Db 61 VLADGALAEVQDQDQAFQVPSVLRKAGQVPMWACVQVITLLVGP 120
QY 213 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 272
Db 61 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 272
QY 121 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 180
Db 121 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 180
QY 273 CQSTVASMHQGVYELKLFNFKALIKGALITFLKALTFVQVROTAFANSTAA 332
Db 181 CQSTVASMHQGVYELKLFNFKALIKGALITFLKALTFVQVROTAFANSTAA 332
QY 333 TNGLVQSLNKKADQVQFNSTENSAASFGTLPALEPQTVTHMPVQIK 392
Db 333 TNGLVQSLNKKADQVQFNSTENSAASFGTLPALEPQTVTHMPVQIK 392
QY 393 ESSSANTTIDE 405
Db 237 ESTESSNTTIDE 249
QY 225 -----ANSLKRP-----DOVK 236
Db 225 -----ANSLKRP-----DOVK 236

RESULT 9
US-10-355-975-10
; Sequence 10, Application US/1095975
; Publication No. US2003004617A9
; APPLICANT: Immunex Corporation
; APPLICANT: Viro, Timothy A.
; APPLICANT: Viro, Timothy A.
; APPLICANT: Martig, Inga
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Anderson, Dirk M.
; FILE REFERENCE: 2021-A
; FILE REFERENCE: 2021-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SEQUENCE CHARACTERISTICS: (Length: 36)
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-355-975-10
Best Local Similarity 35.58; Pred. No. 2,6e+43; Length 355;
Matches 13; Conservative 62; Mismatches 124; Indels 1; Gaps 73;
QY 14 YGVDYGGGSHVYKLVKLTGTAARTINKLAKRQGLKPRFACILKSHN 71
Db 23 PEPFETLGTGSHVYKLVKLTGTAARTINKLAKRQGLKPRFACILKSHN 81
QY 74 VLHSDLSBERTVYDQVGGELVARYTSADASHCTQITLAVLICHQGV 133
Db 83 VALDYSBERTVYDQVGGELVARYTSADASHCTQITLAVLICHQGV 133
QY 134 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 141
Db 141 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 141
QY 142 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 200
Db 142 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 200
QY 194 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 253
Db 194 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 253
QY 201 ATCNGEYVITLLQGTFFPDNDQSLQFLKATFAYEYFQDSDQADPNNLA 260
Db 201 ATCNGEYVITLLQGTFFPDNDQSLQFLKATFAYEYFQDSDQADPNNLA 260
QY 254 TINPARIABALAHKFWCQSTVASMHQGVYELKLFNFKALIKGALIT 301
Db 254 TINPARIABALAHKFWCQSTVASMHQGVYELKLFNFKALIKGALIT 301

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; NAME/SEQ: SITE
; LOCATION: (259)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (260)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-239-953

Query Match
Best Local Similarity 73.54; Pred. No. 1.1e+89;
Matches 230; Conservative 11; Mismatches 8; Indels 64; Gaps 2;
QY 5 VGGSELEPTVARYTSADASHCTQITLAVLICHQGVVDEHGLPNNLLASKKAA 152
Db 1 VTGGSELEPTVARETSADASHCTQITLAVLICHQGVVDEHGLPNNLLASKKAA 60
QY 135 VLADGALAEVQDQDQAFQVPSVLRKAGQVPMWACVQVITLLVGP 212
Db 61 VLADGALAEVQDQDQAFQVPSVLRKAGQVPMWACVQVITLLVGP 120
QY 213 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 272
Db 61 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 272
QY 121 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 180
Db 121 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 180
QY 273 CQSTVASMHQGVYELKLFNFKALIKGALITFLKALTFVQVROTAFANSTAA 332
Db 181 CQSTVASMHQGVYELKLFNFKALIKGALITFLKALTFVQVROTAFANSTAA 332
QY 333 TNGLVQSLNKKADQVQFNSTENSAASFGTLPALEPQTVTHMPVQIK 392
Db 333 TNGLVQSLNKKADQVQFNSTENSAASFGTLPALEPQTVTHMPVQIK 392
QY 393 ESSSANTTIDE 405
Db 237 ESTESSNTTIDE 249
QY 225 -----ANSLKRP-----DOVK 236
Db 225 -----ANSLKRP-----DOVK 236

RESULT 9
US-10-355-975-10
; Sequence 10, Application US/1095975
; Publication No. US2003004617A9
; APPLICANT: Immunex Corporation
; APPLICANT: Viro, Timothy A.
; APPLICANT: Viro, Timothy A.
; APPLICANT: Martig, Inga
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Anderson, Dirk M.
; FILE REFERENCE: 2021-A
; FILE REFERENCE: 2021-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SEQUENCE CHARACTERISTICS: (Length: 36)
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-355-975-10
Best Local Similarity 35.58; Pred. No. 2,6e+43; Length 355;
Matches 13; Conservative 62; Mismatches 124; Indels 1; Gaps 73;
QY 14 YGVDYGGGSHVYKLVKLTGTAARTINKLAKRQGLKPRFACILKSHN 71
Db 23 PEPFETLGTGSHVYKLVKLTGTAARTINKLAKRQGLKPRFACILKSHN 81
QY 74 VLHSDLSBERTVYDQVGGELVARYTSADASHCTQITLAVLICHQGV 133
Db 83 VALDYSBERTVYDQVGGELVARYTSADASHCTQITLAVLICHQGV 133
QY 134 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 141
Db 141 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 141
QY 142 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 200
Db 142 HDGLPNNLLASKKAAVLADGALAEVQDQDQFSPWQVTEKNNLNKQIT 200
QY 194 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 253
Db 194 PWDGSHQALTOQAGQDQFSPWQVTEKNNLNKQITINAKITABALAHNY 253
QY 201 ATCNGEYVITLLQGTFFPDNDQSLQFLKATFAYEYFQDSDQADPNNLA 260
Db 201 ATCNGEYVITLLQGTFFPDNDQSLQFLKATFAYEYFQDSDQADPNNLA 260
QY 254 TINPARIABALAHKFWCQSTVASMHQGVYELKLFNFKALIKGALIT 301
Db 254 TINPARIABALAHKFWCQSTVASMHQGVYELKLFNFKALIKGALIT 301

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Search completed: October 10, 2003, 08:16:23
Job time : 251 secs

Search completed: October 10, 2003, 08:16:23
Job time : 251 secs